

Parameter	Value
Initial temperature	25.0 °C
Final temperature	25.0 °C
Initial pressure	1.00 atm
Final pressure	1.00 atm
Initial volume	1.00 L
Final volume	1.00 L
Initial number of moles	1.00 mol
Final number of moles	1.00 mol
Initial concentration	1.00 mol/L
Final concentration	1.00 mol/L
Initial mass	1.00 g
Final mass	1.00 g
Initial density	1.00 g/L
Final density	1.00 g/L
Initial viscosity	1.00 cP
Final viscosity	1.00 cP
Initial surface tension	1.00 dyne/cm
Final surface tension	1.00 dyne/cm
Initial refractive index	1.00
Final refractive index	1.00
Initial dielectric constant	1.00
Final dielectric constant	1.00
Initial magnetic permeability	1.00
Final magnetic permeability	1.00
Initial electrical conductivity	1.00 S/m
Final electrical conductivity	1.00 S/m
Initial thermal conductivity	1.00 W/m·K
Final thermal conductivity	1.00 W/m·K
Initial specific heat capacity	1.00 J/g·K
Final specific heat capacity	1.00 J/g·K
Initial latent heat of fusion	1.00 J/g
Final latent heat of fusion	1.00 J/g
Initial latent heat of vaporization	1.00 J/g
Final latent heat of vaporization	1.00 J/g
Initial latent heat of sublimation	1.00 J/g
Final latent heat of sublimation	1.00 J/g
Initial enthalpy of formation	1.00 kJ/mol
Final enthalpy of formation	1.00 kJ/mol
Initial Gibbs free energy of formation	1.00 kJ/mol
Final Gibbs free energy of formation	1.00 kJ/mol
Initial Helmholtz free energy of formation	1.00 kJ/mol
Final Helmholtz free energy of formation	1.00 kJ/mol
Initial internal energy of formation	1.00 kJ/mol
Final internal energy of formation	1.00 kJ/mol
Initial enthalpy of combustion	1.00 kJ/mol
Final enthalpy of combustion	1.00 kJ/mol
Initial Gibbs free energy of combustion	1.00 kJ/mol
Final Gibbs free energy of combustion	1.00 kJ/mol
Initial Helmholtz free energy of combustion	1.00 kJ/mol
Final Helmholtz free energy of combustion	1.00 kJ/mol
Initial internal energy of combustion	1.00 kJ/mol
Final internal energy of combustion	1.00 kJ/mol
Initial enthalpy of atomization	1.00 kJ/mol
Final enthalpy of atomization	1.00 kJ/mol
Initial Gibbs free energy of atomization	1.00 kJ/mol
Final Gibbs free energy of atomization	1.00 kJ/mol
Initial Helmholtz free energy of atomization	1.00 kJ/mol
Final Helmholtz free energy of atomization	1.00 kJ/mol
Initial internal energy of atomization	1.00 kJ/mol
Final internal energy of atomization	1.00 kJ/mol
Initial enthalpy of hydration	1.00 kJ/mol
Final enthalpy of hydration	1.00 kJ/mol
Initial Gibbs free energy of hydration	1.00 kJ/mol
Final Gibbs free energy of hydration	1.00 kJ/mol
Initial Helmholtz free energy of hydration	1.00 kJ/mol
Final Helmholtz free energy of hydration	1.00 kJ/mol
Initial internal energy of hydration	1.00 kJ/mol
Final internal energy of hydration	1.00 kJ/mol
Initial enthalpy of solution	1.00 kJ/mol
Final enthalpy of solution	1.00 kJ/mol
Initial Gibbs free energy of solution	1.00 kJ/mol
Final Gibbs free energy of solution	1.00 kJ/mol
Initial Helmholtz free energy of solution	1.00 kJ/mol
Final Helmholtz free energy of solution	1.00 kJ/mol
Initial internal energy of solution	1.00 kJ/mol
Final internal energy of solution	1.00 kJ/mol
Initial enthalpy of mixing	1.00 kJ/mol
Final enthalpy of mixing	1.00 kJ/mol
Initial Gibbs free energy of mixing	1.00 kJ/mol
Final Gibbs free energy of mixing	1.00 kJ/mol
Initial Helmholtz free energy of mixing	1.00 kJ/mol
Final Helmholtz free energy of mixing	1.00 kJ/mol
Initial internal energy of mixing	1.00 kJ/mol
Final internal energy of mixing	1.00 kJ/mol
Initial enthalpy of reaction	1.00 kJ/mol
Final enthalpy of reaction	1.00 kJ/mol
Initial Gibbs free energy of reaction	1.00 kJ/mol
Final Gibbs free energy of reaction	1.00 kJ/mol
Initial Helmholtz free energy of reaction	1.00 kJ/mol
Final Helmholtz free energy of reaction	1.00 kJ/mol
Initial internal energy of reaction	1.00 kJ/mol
Final internal energy of reaction	1.00 kJ/mol

```
Seq. No.          400240
Seq. ID          LIB3431-031-P1-N1-C4
Method          BLASTX
NCBI GI         g132105
BLAST score      653
E value         2.0e-68
Match length    124
% identity      98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                carboxylase S [Oryza sativa]
```

```
Seq. No.      400242
Seq. ID      LIB3431-031-P1-N1-C7
Method       BLASTN
NCBI GI      g2780342
BLAST score   419
E value      0.0e+00
Match length  427
% identity    100
NCBI Description  Oryza sativa gene for PBZ1, complete cds
                >gi_3251321_dbj_E12488_E12488 Nucleotide sequence of Oryza
                sativa PBZ1 gene
```

51241

[illegible]

```
Seq. No.      400293
Seq. ID       LIB3431-033-P1-K1-C9
Method        BLASTX
NCBI GI       g2507455
BLAST score   617
E value       2.0e-64
Match length  141
% identity    82
NCBI Description  FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE
SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir_A43350
formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach
>gi_170145 (M83940) 10-formyltetrahydrofolate synthetase
[Spinacia oleracea]
```

```
Seq. No.      400294
Seq. ID      LIB3431-033-P1-K1-D1
Method       BLASTN
NCBI GI      g3789953
BLAST score   317
E value      1.0e-178
Match length  317
% identity    100
NCBI Description  Oryza sativa chlorophyll a/b-binding protein precursor
                  (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
```

```
Seq. No.      400295
Seq. ID      LIB3431-033-P1-K1-D10
Method       BLASTX
NCBI GI      g3201656
BLAST score   178
E value      6.0e-13
Match length  85
% identity    47
NCBI Description (AF005933) galactokinase [Lactobacillus casei]
```

51252

Seq. ID LIB3431-033-P1-K1-G11
 Method BLASTX
 NCBI GI g3075488
 BLAST score 592
 E value 2.0e-61
 Match length 115
 % identity 96
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 400326
 Seq. ID LIB3431-033-P1-K1-G12
 Method BLASTX
 NCBI GI g4678927
 BLAST score 188
 E value 5.0e-14
 Match length 140
 % identity 37
 NCBI Description (AL049711) hypothetical protein [Arabidopsis thaliana]

Seq. No. 400327
 Seq. ID LIB3431-033-P1-K1-G2
 Method BLASTX
 NCBI GI g4079798
 BLAST score 359
 E value 4.0e-34
 Match length 112
 % identity 67
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 400328
 Seq. ID LIB3431-033-P1-K1-G3
 Method BLASTX
 NCBI GI g2306981
 BLAST score 482
 E value 2.0e-48
 Match length 86
 % identity 98
 NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No. 400329
 Seq. ID LIB3431-033-P1-K1-G4
 Method BLASTX
 NCBI GI g4836892
 BLAST score 427
 E value 3.0e-46
 Match length 136
 % identity 72
 NCBI Description (AC007369) Putative RNA helicase [Arabidopsis thaliana]

Seq. No. 400330
 Seq. ID LIB3431-033-P1-K1-G6
 Method BLASTX
 NCBI GI g1710551
 BLAST score 277
 E value 2.0e-24
 Match length 51


```

NCBI GI      g3789948
BLAST score  167
E value      1.0e-11
Match length 34
% identity   97
NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]

```

```
Seq. No.          400341
Seq. ID           LIB3431-033-P1-N1-A11
Method            BLASTX
NCBI GI           g115784
BLAST score       145
E value           4.0e-09
Match length      26
% identity        100
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I (CAB)
                  (LHCP) >gi_167525 (M16058) chlorophyll a/b-binding protein
                  [Cucumis sativus]
```

```
Seq. No.          400342
Seq. ID           LIB3431-033-P1-N1-A12
Method            BLASTX
NCBI GI           g548603
BLAST score       294
E value           1.0e-26
Match length      57
% identity        96
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir_JQ2247 photosystem I chain D precursor -
                  barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
```

Seq. No.	400343
Seq. ID	LIB3431-033-P1-N1-A3
Method	BLASTN
NCBI GI	g2306980
BLAST score	229
E value	1.0e-126
Match length	254
% identity	98
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

```
Seq. No.      400344
Seq. ID      LIB3431-033-P1-N1-A4
Method       BLASTX
NCBI GI      g2286153
BLAST score   249
E value      2.0e-21
Match length  50
% identity   94
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
```

```
Seq. No.      400345
Seq. ID      LIB3431-033-P1-N1-A5
Method       BLASTN
NCBI GI      q2570514
```


NCBI GI	g4689380
BLAST score	258
E value	3.0e-22
Match length	52
% identity	94
NCBI Description	(AF139465) LHCII type III chlorophyll a/b binding protein [Vigna radiata]

Seq. No.	400391
Seq. ID	LIB3431-033-P1-N1-H4
Method	BLASTN
NCBI GI	g2072554
BLAST score	290
E value	1.0e-162
Match length	294
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

```
Seq. No.      400392
Seq. ID      LIB3431-033-P1-N1-H7
Method       BLASTX
NCBI GI      g132105
BLAST score   301
E value      2.0e-27
Match length  57
% identity    100
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                carboxylase S [Oryza sativa]
```

```
Seq. No.          400393
Seq. ID           LIB3431-033-P1-N1-H9
Method            BLASTX
NCBI GI           g170131
BLAST score       152
E value           6.0e-10
Match length      47
% identity        64
NCBI Description  (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
```

Seq. No.	400394
Seq. ID	LIB3431-034-P1-K1-A11
Method	BLASTX
NCBI GI	g4469021
BLAST score	268
E value	2.0e-23
Match length	78
% identity	69
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. ID	LIB3431-034-P1-K1-G12
Method	BLASTN
NCBI GI	g6015437
BLAST score	34
E value	2.0e-10
Match length	38
% identity	97
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

```
Seq. No.      400444
Seq. ID      LIB3431-034-P1-K1-G3
Method       BLASTX
NCBI GI      g4079798
BLAST score   338
E value      1.0e-31
Match length 110
% identity   63
NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza
sativa]
```

```
Seq. No.      400445
Seq. ID      LIB3431-034-P1-K1-G4
Method       BLASTX
NCBI GI      g3319357
BLAST score   374
E value      7.0e-36
Match length  118
% identity    67
NCBI Description (AF077407) contains similarity to phosphoenolpyruvate
synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
```

```
Seq. No.      400446
Seq. ID      LIB3431-034-P1-K1-G5
Method       BLASTX
NCBI GI      g3126854
BLAST score   675
E value      4.0e-71
Match length  127
% identity    100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.          400447
Seq. ID           LIB3431-034-P1-K1-G7
Method            BLASTN
NCBI GI           g6015437
BLAST score       35
E value           2.0e-10
Match length      35
% identity        100
NCBI Description  Homo sapiens PEX1 mRNA, complete cds
```

```
Seq. No.      400448
Seq. ID      LIB3431-034-P1-K1-H1
Method       BLASTX
NCBI GI      g2288988
BLAST score   170
E value      6.0e-12
```


Seq. No. 400483
 Seq. ID LIB3431-034-P1-N1-E11
 Method BLASTX
 NCBI GI g1181599
 BLAST score 144
 E value 5.0e-09
 Match length 39
 % identity 72
 NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]

Seq. No. 400484
 Seq. ID LIB3431-034-P1-N1-E12
 Method BLASTX
 NCBI GI g5902389
 BLAST score 170
 E value 5.0e-12
 Match length 49
 % identity 55
 NCBI Description (AC008148) Unknown protein [Arabidopsis thaliana]

Seq. No. 400485
 Seq. ID LIB3431-034-P1-N1-E2
 Method BLASTN
 NCBI GI g1209384
 BLAST score 337
 E value 0.0e+00
 Match length 341
 % identity 100
 NCBI Description Oryza sativa mRNA for root ferredoxin, partial cds

Seq. No. 400486
 Seq. ID LIB3431-034-P1-N1-E4
 Method BLASTN
 NCBI GI g4887617
 BLAST score 434
 E value 0.0e+00
 Match length 449
 % identity 99
 NCBI Description Oryza sativa HOS59 mRNA, partial cds

Seq. No. 400487
 Seq. ID LIB3431-034-P1-N1-E5
 Method BLASTX
 NCBI GI g2204226
 BLAST score 255
 E value 6.0e-22
 Match length 55
 % identity 82
 NCBI Description (Y13848) alpha-galactosidase [Hordeum vulgare]

Seq. No. 400488
 Seq. ID LIB3431-034-P1-N1-F1
 Method BLASTX
 NCBI GI g3036949
 BLAST score 234
 E value 1.0e-19

% identity	75
NCBI Description	PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir_JQ2254 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta chain - garden pea >gi_169049 (L08664) farnesyl-protein transferase beta-subunit [Pisum sativum]

```
Seq. No.      400504
Seq. ID      LIB3431-034-P1-N1-H4
Method       BLASTN
NCBI GI      g3819197
BLAST score   47
E value      4.0e-17
Match length  103
% identity    86
NCBI Description  Hordeum vulgare partial mRNA; clone cMWG0676.uni
```

```
Seq. No.      400505
Seq. ID      LIB3431-034-P1-N1-H7
Method       BLASTN
NCBI GI      g218207
BLAST score   295
E value      1.0e-165
Match length  307
% identity    99
NCBI Description  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS1139
```

```
Seq. No.      400506
Seq. ID      LIB3431-035-P1-K1-A1
Method       BLASTX
NCBI GI      g548605
BLAST score   471
E value      3.0e-47
Match length  98
% identity    93
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                >gi_539055_pir_A48527 photosystem I protein psaK precursor
                - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                [Hordeum vulgare]
```

```
Seq. No.      400507
Seq. ID      LIB3431-035-P1-K1-A12
Method       BLASTX
NCBI GI      g1171579
BLAST score   239
E value      5.0e-20
Match length  91
% identity    48
NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]
```

Seq. No.	400508
Seq. ID	LIB3431-035-P1-K1-A2
Method	BLASTX


```

NCBI GI          g82080
BLAST score      483
E value          1.0e-48
Match length     134
% identity       69
NCBI Description  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf_1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]

```

```
Seq. No.      400528
Seq. ID      LIB3431-035-P1-K1-D11
Method       BLASTX
NCBI GI      g170131
BLAST score   263
E value      8.0e-23
Match length  67
% identity    67
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
```

```
Seq. No.          400529
Seq. ID           LIB3431-035-P1-K1-D12
Method            BLASTX
NCBI GI           g2773154
BLAST score       242
E value           2.0e-20
Match length      118
% identity        47
NCBI Description   (AF039573) abscisic acid- and stress-inducible protein
                  [Oryza sativa]
```

```
Seq. No.      400530
Seq. ID      LIB3431-035-P1-K1-D2
Method       BLASTX
NCBI GI      g3126854
BLAST score   744
E value      3.0e-79
Match length  141
% identity    99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.      400531
Seq. ID      LIB3431-035-P1-K1-D3
Method       BLASTX
NCBI GI      g6014904
BLAST score   372
E value      1.0e-35
Match length  70
% identity    97
NCBI Description  DAG PROTEIN, CHLOROPLAST PRECURSOR
                >gi 1200205 emb CAA65064 (X95753) DAG [Antirrhinum majus]
```

```
Seq. No.      400532
Seq. ID       LIB3431-035-P1-K1-D4
Method        BLASTX
NCBI GI       g3789952
BLAST score   512
E value       4.0e-52
```


Match length 108
 % identity 94
 NCBI Description (AF094775) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 400533
 Seq. ID LIB3431-035-P1-K1-D5
 Method BLASTX
 NCBI GI g543711
 BLAST score 367
 E value 5.0e-35
 Match length 71
 % identity 99
 NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796_pir_S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140) brain specific protein [Oryza sativa]

Seq. No. 400534
 Seq. ID LIB3431-035-P1-K1-D6
 Method BLASTX
 NCBI GI g1172874
 BLAST score 204
 E value 7.0e-16
 Match length 135
 % identity 38
 NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi_479589_pir_S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf_1913421A rd22 gene [Arabidopsis thaliana]

Seq. No. 400535
 Seq. ID LIB3431-035-P1-K1-D8
 Method BLASTX
 NCBI GI g132105
 BLAST score 673
 E value 7.0e-71
 Match length 124
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400536
 Seq. ID LIB3431-035-P1-K1-E1
 Method BLASTX
 NCBI GI g320618
 BLAST score 544
 E value 1.0e-55
 Match length 128
 % identity 84


```
% identity      80
NCBI Description (U49387) adenylosuccinate synthetase [Triticum aestivum]
```

```
Seq. No.      400557
Seq. ID      LIB3431-035-P1-K1-G5
Method       BLASTX
NCBI GI      g5031281
BLAST score   314
E value      9.0e-29
Match length  98
% identity    62
NCBI Description (AF139499) unknown [Prunus armeniaca]
```

Seq. No.	400558
Seq. ID	LIB3431-035-P1-K1-G6
Method	BLASTN
NCBI GI	g1245938
BLAST score	35
E value	6.0e-10
Match length	35
% identity	100
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	400559
Seq. ID	LIB3431-035-P1-K1-G8
Method	BLASTX
NCBI GI	g3885888
BLAST score	347
E value	1.0e-32
Match length	70
% identity	97
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

```
Seq. No.      400560
Seq. ID      LIB3431-035-P1-K1-G9
Method       BLASTX
NCBI GI      g422029
BLAST score   542
E value      2.0e-55
Match length  150
% identity    73
NCBI Description transcription factor OBF3.2, ocs element-binding - maize
              >gi_297018_emb_CAA48904_ (X69152) ocs-element binding
              factor 3.2 [Zea mays]
```

```
Seq. No.      400561
Seq. ID       LIB3431-035-P1-K1-H1
Method        BLASTX
NCBI GI       g2407281
BLAST score    705
E value       1.0e-74
Match length  132
% identity    99
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
subunit [Oryza sativa]
```


Seq. ID LIB3431-035-P1-N1-A2
 Method BLASTX
 NCBI GI g2582822
 BLAST score 169
 E value 6.0e-12
 Match length 39
 % identity 79
 NCBI Description (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No. 400572
 Seq. ID LIB3431-035-P1-N1-B3
 Method BLASTX
 NCBI GI g115787
 BLAST score 368
 E value 3.0e-35
 Match length 73
 % identity 97
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 400573
 Seq. ID LIB3431-035-P1-N1-B8
 Method BLASTX
 NCBI GI g417488
 BLAST score 184
 E value 9.0e-19
 Match length 60
 % identity 82
 NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi_100452_pir_A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi_169473 (M69038) alpha-glucan phosphorylase type H isozyme [Solanum tuberosum]

Seq. No. 400574
 Seq. ID LIB3431-035-P1-N1-B9
 Method BLASTX
 NCBI GI g1085987
 BLAST score 179
 E value 4.0e-13
 Match length 34
 % identity 94
 NCBI Description light harvesting chlorophyll a protein precursor - Norway spruce >gi_607148_emb_CAA57407_ (X81808) light harvesting chlorophyll a /b-binding protein Lhcb1*1 [Picea abies]

Seq. No. 400575
 Seq. ID LIB3431-035-P1-N1-C11
 Method BLASTX
 NCBI GI g671740
 BLAST score 406
 E value 1.0e-39
 Match length 79
 % identity 96

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

```
Seq. No.          400576
Seq. ID           LIB3431-035-P1-N1-C2
Method            BLASTX
NCBI GI           g482311
BLAST score       171
E value           4.0e-12
Match length      33
% identity         100
NCBI Description  photosystem II oxygen-evolving complex protein 1 - rice
                  (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
```

Seq. No.	400577
Seq. ID	LIB3431-035-P1-N1-C3
Method	BLASTX
NCBI GI	g1362150
BLAST score	290
E value	1.0e-33
Match length	84
% identity	88
NCBI Description	hypothetical protein (clone AFN3) - wild oat (fragment) >gi 726478 (U20000) putative ORF1 [Avena fatua]

Seq. No.	400578
Seq. ID	LIB3431-035-P1-N1-C4
Method	BLASTN
NCBI GI	g2331130
BLAST score	227
E value	1.0e-125
Match length	251
% identity	98
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No.	400579
Seq. ID	LIB3431-035-P1-N1-C7
Method	BLASTN
NCBI GI	g218209
BLAST score	57
E value	3.0e-23
Match length	172
% identity	90
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

```
Seq. No.          400580
Seq. ID           LIB3431-035-P1-N1-C8
Method            BLASTN
NCBI GI           g5042437
BLAST score       325
E value           0.0e+00
Match length      389
% identity        100
```


% identity	98
NCBI Description	Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds
Seq. No.	400586
Seq. ID	LIB3431-035-P1-N1-D2
Method	BLASTN
NCBI GI	g3126853
BLAST score	160
E value	1.0e-84
Match length	210
% identity	99
NCBI Description	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds
Seq. No.	400587
Seq. ID	LIB3431-035-P1-N1-D4
Method	BLASTX
NCBI GI	g3789952
BLAST score	168
E value	1.0e-11
Match length	30
% identity	100
NCBI Description	(AF094775) chlorophyll a/b-binding protein precursor [Oryza sativa]
Seq. No.	400588
Seq. ID	LIB3431-035-P1-N1-D5
Method	BLASTX
NCBI GI	g543711
BLAST score	367
E value	6.0e-35
Match length	71
% identity	99
NCBI Description	14-3-3-LIKE PROTEIN S94 >gi_419796_pir_S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140) brain specific protein [Oryza sativa]
Seq. No.	400589
Seq. ID	LIB3431-035-P1-N1-D8
Method	BLASTN
NCBI GI	g218209
BLAST score	34
E value	2.0e-09
Match length	50
% identity	92
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106
Seq. No.	400590
Seq. ID	LIB3431-035-P1-N1-D9
Method	BLASTX
NCBI GI	g259138
BLAST score	242
E value	2.0e-20

Match length	45
% identity	100
NCBI Description	oryzacystatin=cysteine protease inhibitor [Oryza=rice, Peptide Recombinant, 90 aa]
Seq. No.	400591
Seq. ID	LIB3431-035-P1-N1-E1
Method	BLASTX
NCBI GI	g115787
BLAST score	410
E value	4.0e-40
Match length	77
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]
Seq. No.	400592
Seq. ID	LIB3431-035-P1-N1-E10
Method	BLASTX
NCBI GI	g1617197
BLAST score	286
E value	2.0e-25
Match length	71
% identity	73
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]
Seq. No.	400593
Seq. ID	LIB3431-035-P1-N1-E11
Method	BLASTX
NCBI GI	g1076724
BLAST score	263
E value	6.0e-23
Match length	51
% identity	96
NCBI Description	LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]
Seq. No.	400594
Seq. ID	LIB3431-035-P1-N1-E2
Method	BLASTX
NCBI GI	g2464852
BLAST score	171
E value	5.0e-12
Match length	80
% identity	49
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]
Seq. No.	400595
Seq. ID	LIB3431-035-P1-N1-E4
Method	BLASTX
NCBI GI	g115794
BLAST score	467
E value	1.0e-46


```

Match length      94
% identity        91
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
                  III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
                  >gi_19277_emb_CAA42818_ (X60275) LHCII type III
                  [Lycopersicon esculentum]

```

```
Seq. No.          400596
Seq. ID           LIB3431-035-P1-N1-E6
Method            BLASTX
NCBI GI           g115768
BLAST score       223
E value           4.0e-18
Match length      43
% identity        98
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB) (LHCP) >gi_72743_pir_CDKV chlorophyll a/b-binding
                  protein precursor - cucumber (fragment) >gi_167523 (M16057)
                  chlorophyll a/b-binding protein [Cucumis sativus]
```

Seq. No.	400597
Seq. ID	LIB3431-035-P1-N1-E9
Method	BLASTX
NCBI GI	g2582822
BLAST score	362
E value	2.0e-34
Match length	79
% identity	85
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No.	400598
Seq. ID	LIB3431-035-P1-N1-F1
Method	BLASTX
NCBI GI	g671737
BLAST score	199
E value	2.0e-15
Match length	37
% identity	100
NCBI Description	(X74731) Chlorophyll a/b binding protein [Amaranthus hypochondriacus]

```
Seq. No.      400599
Seq. ID      LIB3431-035-P1-N1-F10
Method       BLASTX
NCBI GI      g115813
BLAST score   230
E value      6.0e-19
Match length  55
% identity    82
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
```

Seq. No.	400600
Seq. ID	LIB3431-035-P1-N1-F7

[illegible]


```
BLAST score      289
E value         6.0e-26
Match length    62
% identity      92
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                [Zea mays]
```

```
Seq. No.      400606
Seq. ID      LIB3431-035-P1-N1-G3
Method       BLASTX
NCBI GI      g2462750
BLAST score   184
E value      1.0e-13
Match length  53
% identity    68
NCBI Description (AC002292) Highly similar to auxin-induced protein
                (aldo/keto reductase family) [Arabidopsis thaliana]
```

```
Seq. No.          400607
Seq. ID           LIB3431-035-P1-N1-G4
Method            BLASTX
NCBI GI           g1616659
BLAST score       343
E value           4.0e-32
Match length      75
% identity        88
NCBI Description   (U49387) adenylosuccinate synthetase [Triticum aestivum]
```

```
Seq. No.      400608
Seq. ID      LIB3431-035-P1-N1-G8
Method       BLASTN
NCBI GI      g3885887
BLAST score   304
E value      1.0e-170
Match length  315
% identity    99
NCBI Description  Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
```

Seq. No.	400609
Seq. ID	LIB3431-035-P1-N1-H1
Method	BLASTN
NCBI GI	g218209
BLAST score	152
E value	7.0e-80
Match length	343
% identity	97
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	400610
Seq. ID	LIB3431-035-P1-N1-H10
Method	BLASTX
NCBI GI	g347451
BLAST score	380
E value	2.0e-36


```

Match length      42
% identity        79
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]

```

Seq. No.	400616
Seq. ID	LIB3431-036-P1-K1-A1
Method	BLASTX
NCBI GI	g2997684
BLAST score	245
E value	1.0e-20
Match length	85
% identity	56
NCBI Description	(AF053302) putative transcriptional co-activator [Arabidopsis thaliana]

```
Seq. No.          400617
Seq. ID           LIB3431-036-P1-K1-A11
Method            BLASTX
NCBI GI           g2072555
BLAST score       237
E value           9.0e-20
Match length      44
% identity         100
NCBI Description  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
```

Seq. No.	400618
Seq. ID	LIB3431-036-P1-K1-A12
Method	BLASTX
NCBI GI	g871931
BLAST score	399
E value	7.0e-39
Match length	95
% identity	86
NCBI Description	(D30763) ferredoxin [Oryza sativa]

```
Seq. No.      400619
Seq. ID      LIB3431-036-P1-K1-A4
Method       BLASTX
NCBI GI      g1709846
BLAST score   180
E value      4.0e-13
Match length  122
% identity    47
NCBI Description  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336)
                22 kDa component of photosystem II [Lycopersicon
                esculentum]
```

```
Seq. No.      400620
Seq. ID      LIB3431-036-P1-K1-A5
Method       BLASTN
NCBI GI      g6016845
BLAST score   301
E value      1.0e-168
```


Regression Statistics					
R	0.99				
R Square	0.98				
Adjusted R Square	0.97				
Standard Error	0.0001				
ANOVA					
	df	SS	MS	F	Significance F
Regression	1	0.9999	0.9999	158.65	0.0000
Residual	1	0.0001	0.0001		
Total	2	1.0000			
Coefficients					
	Intercept	Variable1			
Intercept	0.0000	0.9999			
Variable1	0.9999	0.0000			
t-Statistic					
	Intercept	Variable1			
Intercept	0.0000	0.9999			
Variable1	0.9999	0.0000			
P-Value					
	Intercept	Variable1			
Intercept	0.0000	0.9999			
Variable1	0.9999	0.0000			
Standardized Coefficients					
	Intercept	Variable1			
Intercept	0.0000	0.9999			
Variable1	0.9999	0.0000			
Durbin-Watson					
Durbin-Watson	1.9999				
Serial Correlation	0.0000				
Autocorrelation	0.0000				
Partial Correlation	0.9999				
Partial Correlation Squared	0.9999				
Partial Correlation Cubed	0.9999				
Partial Correlation Fourth	0.9999				
Partial Correlation Fifth	0.9999				
Partial Correlation Sixth	0.9999				
Partial Correlation Seventh	0.9999				
Partial Correlation Eighth	0.9999				
Partial Correlation Ninth	0.9999				
Partial Correlation Tenth	0.9999				
Partial Correlation Eleventh	0.9999				
Partial Correlation Twelfth	0.9999				
Partial Correlation Thirteenth	0.9999				
Partial Correlation Fourteenth	0.9999				
Partial Correlation Fifteenth	0.9999				
Partial Correlation Sixteenth	0.9999				
Partial Correlation Seventeenth	0.9999				
Partial Correlation Eighteenth	0.9999				
Partial Correlation Nineteenth	0.9999				
Partial Correlation Twentieth	0.9999				
Partial Correlation Twenty-first	0.9999				
Partial Correlation Twenty-second	0.9999				
Partial Correlation Twenty-third	0.9999				
Partial Correlation Twenty-fourth	0.9999				
Partial Correlation Twenty-fifth	0.9999				
Partial Correlation Twenty-sixth	0.9999				
Partial Correlation Twenty-seventh	0.9999				
Partial Correlation Twenty-eighth	0.9999				
Partial Correlation Twenty-ninth	0.9999				
Partial Correlation Thirtieth	0.9999				
Partial Correlation Thirty-first	0.9999				
Partial Correlation Thirty-second	0.9999				
Partial Correlation Thirty-third	0.9999				
Partial Correlation Thirty-fourth	0.9999				
Partial Correlation Thirty-fifth	0.9999				
Partial Correlation Thirty-sixth	0.9999				
Partial Correlation Thirty-seventh	0.9999				
Partial Correlation Thirty-eighth	0.9999				
Partial Correlation Thirty-ninth	0.9999				
Partial Correlation Fortieth	0.9999				
Partial Correlation Forty-first	0.9999				
Partial Correlation Forty-second	0.9999				
Partial Correlation Forty-third	0.9999				
Partial Correlation Forty-fourth	0.9999				
Partial Correlation Forty-fifth	0.9999				
Partial Correlation Forty-sixth	0.9999				
Partial Correlation Forty-seventh	0.9999				
Partial Correlation Forty-eighth	0.9999				
Partial Correlation Forty-ninth	0.9999				
Partial Correlation Fiftieth	0.9999				
Partial Correlation Fifty-first	0.9999				
Partial Correlation Fifty-second	0.9999				
Partial Correlation Fifty-third	0.9999				
Partial Correlation Fifty-fourth	0.9999				
Partial Correlation Fifty-fifth	0.9999				
Partial Correlation Fifty-sixth	0.9999				
Partial Correlation Fifty-seventh	0.9999				
Partial Correlation Fifty-eighth	0.9999				
Partial Correlation Fifty-ninth	0.9999				
Partial Correlation Sixtieth	0.9999				
Partial Correlation Sixty-first	0.9999				
Partial Correlation Sixty-second	0.9999				
Partial Correlation Sixty-third	0.9999				
Partial Correlation Sixty-fourth	0.9999				
Partial Correlation Sixty-fifth	0.9999				
Partial Correlation Sixty-sixth	0.9999				
Partial Correlation Sixty-seventh	0.9999				
Partial Correlation Sixty-eighth	0.9999				
Partial Correlation Sixty-ninth	0.9999				
Partial Correlation Seventieth	0.9999				
Partial Correlation Seventy-first	0.9999				
Partial Correlation Seventy-second	0.9999				
Partial Correlation Seventy-third	0.9999				
Partial Correlation Seventy-fourth	0.9999				
Partial Correlation Seventy-fifth	0.9999				
Partial Correlation Seventy-sixth	0.9999				
Partial Correlation Seventy-seventh	0.9999				
Partial Correlation Seventy-eighth	0.9999				
Partial Correlation Seventy-ninth	0.9999				
Partial Correlation Eightieth	0.9999				
Partial Correlation Eighty-first	0.9999				
Partial Correlation Eighty-second	0.9999				
Partial Correlation Eighty-third	0.9999				
Partial Correlation Eighty-fourth	0.9999				
Partial Correlation Eighty-fifth	0.9999				
Partial Correlation Eighty-sixth	0.9999				
Partial Correlation Eighty-seventh	0.9999				
Partial Correlation Eighty-eighth	0.9999				
Partial Correlation Eighty-ninth	0.9999				
Partial Correlation Ninetieth	0.9999				
Partial Correlation Ninety-first	0.9999				
Partial Correlation Ninety-second	0.9999				
Partial Correlation Ninety-third	0.9999				
Partial Correlation Ninety-fourth	0.9999				
Partial Correlation Ninety-fifth	0.9999				
Partial Correlation Ninety-sixth	0.9999				
Partial Correlation Ninety-seventh	0.9999				
Partial Correlation Ninety-eighth	0.9999				
Partial Correlation Ninety-ninth	0.9999				
Partial Correlation One Hundred	0.9999				

```
Seq. No.      400631
Seq. ID      LIB3431-036-P1-K1-B9
Method       BLASTX
NCBI GI      g320618
BLAST score   486
E value      5.0e-49
Match length  111
% identity    84
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]
```

Seq. No.	400633
Seq. ID	LIB3431-036-P1-K1-C11
Method	BLASTX
NCBI GI	g3126854
BLAST score	715
E value	7.0e-76
Match length	136
% identity	99
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

51321

E value	7.0e-34
Match length	75
% identity	88
NCBI Description	PROTEASOME DELTA CHAIN PRECURSOR (MULTICATALYTIC ENDOPEPTIDASE COMPLEX DELTA CHAIN) >gi_1743356_emb_CAA70699_ (Y09505) proteasome delta subunit [Nicotiana tabacum]

```
Seq. No.      400640
Seq. ID      LIB3431-036-P1-K1-D1
Method       BLASTX
NCBI GI      g4105561
BLAST score   186
E value      8.0e-14
Match length  80
% identity    54
NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
```

```
Seq. No.          400641
Seq. ID           LIB3431-036-P1-K1-D10
Method            BLASTX
NCBI GI           gi115787
BLAST score       592
E value           5.0e-64
Match length      133
% identity        94
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

```
Seq. No.      400642
Seq. ID      LIB3431-036-P1-K1-D11
Method       BLASTX
NCBI GI      g131388
BLAST score   283
E value      3.0e-25
Match length  107
% identity    63
NCBI Description  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260
photosystem II oxygen-evolving complex protein 1 - common
wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
33kDa oxygen evolving protein of photosystem II [Triticum
aestivum]
```

```
Seq. No.          400643
Seq. ID           LIB3431-036-P1-K1-D3
Method            BLASTX
NCBI GI           g4759278
BLAST score       301
E value           3.0e-27
Match length      144
% identity        43
NCBI Description   prp28, U5 snRNP 100 kd protein >gi 2655202 (AF026402) U5
```



```
BLAST score      237
E value          9.0e-20
Match length     44
% identity       100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]
```

```
Seq. No.      400660
Seq. ID      LIB3431-036-P1-K1-F12
Method       BLASTN
NCBI GI      g1245938
BLAST score   36
E value      1.0e-10
Match length  36
% identity    100
NCBI Description rabClc-2 beta=chloride channel ClC-2G isoform [rabbits,
heart atrium, mRNA, 2998 nt]
```

```
Seq. No.      400661
Seq. ID       LIB3431-036-P1-K1-F2
Method        BLASTX
NCBI GI       g6017100
BLAST score   588
E value       6.0e-61
Match length  142
% identity    71
NCBI Description (AC009895) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      400662
Seq. ID      LIB3431-036-P1-K1-F3
Method       BLASTX
NCBI GI      g131388
BLAST score   383
E value      6.0e-37
Match length  127
% identity    66
NCBI Description  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260
photosystem II oxygen-evolving complex protein 1 - common
wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
33kDa oxygen evolving protein of photosystem II [Triticum
aestivum]
```

Seq. No.	400663
Seq. ID	LIB3431-036-P1-K1-F4
Method	BLASTX
NCBI GI	g3789952
BLAST score	275
E value	3.0e-24
Match length	55
% identity	96
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No. 400664

Seq. No. 400684
 Seq. ID LIB3431-036-P1-N1-A8
 Method BLASTX
 NCBI GI g132105
 BLAST score 402
 E value 4.0e-39
 Match length 73
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 400685
 Seq. ID LIB3431-036-P1-N1-A9
 Method BLASTX
 NCBI GI g730456
 BLAST score 335
 E value 3.0e-31
 Match length 65
 % identity 100
 NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 400686
 Seq. ID LIB3431-036-P1-N1-B12
 Method BLASTX
 NCBI GI g671740
 BLAST score 532
 E value 2.0e-54
 Match length 103
 % identity 95
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 400687
 Seq. ID LIB3431-036-P1-N1-B2
 Method BLASTX
 NCBI GI g3914466
 BLAST score 369
 E value 3.0e-35
 Match length 67
 % identity 99
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
 (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
 subunit precursor [Zea mays]

Seq. No. 400688
 Seq. ID LIB3431-036-P1-N1-B3
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237


```
E value          1.0e-19
Match length     44
% identity       100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]
```

Seq. No.	400689
Seq. ID	LIB3431-036-P1-N1-B4
Method	BLASTX
NCBI GI	g2306981
BLAST score	236
E value	1.0e-19
Match length	52
% identity	87
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]

```
Seq. No.      400690
Seq. ID      LIB3431-036-P1-N1-B5
Method       BLASTX
NCBI GI      g132105
BLAST score   443
E value      7.0e-44
Match length  80
% identity    100
NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                carboxylase S [Oryza sativa]
```

```
Seq. No.      400691
Seq. ID      LIB3431-036-P1-N1-B6
Method       BLASTX
NCBI GI      g4760553
BLAST score   429
E value      3.0e-42
Match length  82
% identity    95
NCBI Description (AB019533) Nad-dependent formate dehydrogenase [Oryza
sativa]
```

```
Seq. No.      400692
Seq. ID      LIB3431-036-P1-N1-B7
Method       BLASTX
NCBI GI      g115794
BLAST score   550
E value      2.0e-56
Match length  111
% identity    94
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding
protein type III precursor (cab-13) - tomato
```


% identity	92
NCBI Description	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi_100555_pir_A39356 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) I beta chain precursor, chloroplast - barley >gi_167065 (M60410) beta-ketoacyl-ACP synthase I [Hordeum vulgare]
Seq. No.	400698
Seq. ID	LIB3431-036-P1-N1-C9
Method	BLASTX
NCBI GI	g2511594
BLAST score	326
E value	4.0e-30
Match length	95
% identity	66
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_2827525_emb_CAA16533.1 (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]
Seq. No.	400699
Seq. ID	LIB3431-036-P1-N1-D1
Method	BLASTX
NCBI GI	g4105561
BLAST score	391
E value	9.0e-38
Match length	85
% identity	88
NCBI Description	(AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
Seq. No.	400700
Seq. ID	LIB3431-036-P1-N1-D10
Method	BLASTX
NCBI GI	g3036942
BLAST score	363
E value	2.0e-34
Match length	71
% identity	97
NCBI Description	(AB012636) light harvesting chlorophyll a/b-binding protein [Nicotiana glauca]
Seq. No.	400701
Seq. ID	LIB3431-036-P1-N1-D11
Method	BLASTX
NCBI GI	g482311
BLAST score	428
E value	4.0e-42
Match length	86
% identity	99
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]
Seq. No.	400702


```
Match length      83
% identity        67
NCBI Description  (AC006341) ESTs gb_N38586 and gb_N38613 come from this
                  gene. [Arabidopsis thaliana]
```

```
Seq. No.      400708
Seq. ID      LIB3431-036-P1-N1-E5
Method       BLASTX
NCBI GI      g3047125
BLAST score   205
E value      6.0e-16
Match length  75
% identity    48
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
```

```
Seq. No.      400709
Seq. ID      LIB3431-036-P1-N1-E8
Method       BLASTX
NCBI GI      g3461848
BLAST score   210
E value      1.0e-16
Match length  75
% identity    64
NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]
```

```
Seq. No.      400710
Seq. ID       LIB3431-036-P1-N1-F1
Method        BLASTX
NCBI GI       g1071913
BLAST score   365
E value       1.0e-34
Match length  103
% identity    70
NCBI Description cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
                - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine
                synthase [Spinacia oleracea]
```

```
Seq. No.      400711
Seq. ID      LIB3431-036-P1-N1-F10
Method       BLASTX
NCBI GI      g461595
BLAST score   220
E value      9.0e-18
Match length  98
% identity    49
NCBI Description  ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II)
                >gi_479533_pir_S34473 H+-transporting ATP synthase (EC
                3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520_
                (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]
```

```
Seq. No.      400712
Seq. ID      LIB3431-036-P1-N1-F11
Method       BLASTX
NCBI GI      g2072555
BLAST score   237
E value      1.0e-19
Match length  44
```



```
Seq. No.      400733
Seq. ID      LIB3431-036-P1-N1-H8
Method       BLASTX
NCBI GI      g548605
BLAST score   473
E value      2.0e-47
Match length  113
% identity    85
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                >gi_539055_pir_A48527 photosystem I protein psaK precursor
                - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                [Hordeum vulgare]
```

```
Seq. No.      400734
Seq. ID      LIB3431-037-P1-K1-A1
Method       BLASTX
NCBI GI      g671740
BLAST score   471
E value      2.0e-47
Match length  89
% identity    97
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]
```

```
Seq. No.      400735
Seq. ID      LIB3431-037-P1-K1-A11
Method       BLASTX
NCBI GI      g5262946
BLAST score   661
E value      2.0e-69
Match length  149
% identity    79
NCBI Description (Y19104) beta-alanine synthase [Lycopersicon esculentum]
```

```
Seq. No.      400736
Seq. ID      LIB3431-037-P1-K1-A12
Method       BLASTX
NCBI GI      g2984709
BLAST score   154
E value      1.0e-12
Match length  105
% identity    49
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
```

```
Seq. No.      400737
Seq. ID      LIB3431-037-P1-K1-A4
Method       BLASTX
NCBI GI      g4996105
BLAST score   386
E value      3.0e-37
Match length  93
% identity    76
NCBI Description (AB014076) histidine decarboxylase [Brassica napus]
```

Seq. No. 400738

1. Demographic Data	
Age	25.5
Gender	Male
Education	High School
Occupation	Student
Marital Status	Single
Religion	Christian
Ethnicity	White
Income	\$15,000
Health Status	Good
Smoking Status	Non-smoker
Alcohol Consumption	Occasional
Exercise Frequency	Weekly
Stress Level	Low
Sleep Quality	Good
Dietary Habits	Healthy
Family Size	2
Home Ownership	Rent
Vehicle Ownership	Yes
Travel Frequency	Monthly
Communication Skills	Good
Problem Solving Skills	Good
Emotional Stability	Good
Self-esteem	Good
Life Satisfaction	Good
Overall Health	Good


```

NCBI GI          g132105
BLAST score      614
E value          6.0e-64
Match length     132
% identity       88
NCBI Description  RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose biphosphate
                  carboxylase S [Oryza sativa]

```

```
Seq. No.          400743
Seq. ID          LIB3431-037-P1-K1-B12
Method           BLASTX
NCBI GI          g3377815
BLAST score      258
E value          3.0e-22
Match length     76
% identity       68
NCBI Description (AF076275) similar to protein kinases (Pfam: pkinase.hmm,
score: 255.71) [Arabidopsis thaliana]
```

```
Seq. No.      400744
Seq. ID      LIB3431-037-P1-K1-B2
Method       BLASTX
NCBI GI      g115787
BLAST score   558
E value      2.0e-57
Match length  140
% identity    81
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

Seq. No.	400745
Seq. ID	LIB3431-037-P1-K1-B3
Method	BLASTN
NCBI GI	g3885891
BLAST score	129
E value	2.0e-66
Match length	182
% identity	99
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

```
Seq. No.          400746
Seq. ID           LIB3431-037-P1-K1-B4
Method            BLASTX
NCBI GI           g3789954
BLAST score       388
E value           2.0e-37
```


% identity 39
NCBI Description (AF028842) DegP protease precursor [Arabidopsis thaliana]

Seq. No. 400789
Seq. ID LIB3431-037-P1-K1-G5
Method BLASTX
NCBI GI g1708191
BLAST score 428
E value 4.0e-42
Match length 135
% identity 55

NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose carrier protein [Ricinus communis]

Seq. No. 400790
Seq. ID LIB3431-037-P1-K1-G7
Method BLASTX
NCBI GI g548603
BLAST score 698
E value 2.0e-75
Match length 148
% identity 97

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir_JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 400791
Seq. ID LIB3431-037-P1-K1-G8
Method BLASTX
NCBI GI g3603401
BLAST score 414
E value 2.0e-40
Match length 131
% identity 61

NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No. 400792
Seq. ID LIB3431-037-P1-K1-G9
Method BLASTX
NCBI GI g320618
BLAST score 546
E value 6.0e-56
Match length 123
% identity 85

NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 400793
Seq. ID LIB3431-037-P1-K1-H1
Method BLASTX
NCBI GI g3294467
BLAST score 682
E value 6.0e-72

Seq. No. 400818
 Seq. ID LIB3431-037-P1-N1-D11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 345
 E value 2.0e-32
 Match length 65
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [*Oryza sativa*]

Seq. No. 400819
 Seq. ID LIB3431-037-P1-N1-D12
 Method BLASTX
 NCBI GI g3036942
 BLAST score 216
 E value 2.0e-17
 Match length 45
 % identity 89
 NCBI Description (AB012636) light harvesting chlorophyll a/b-binding protein [*Nicotiana glauca*]

Seq. No. 400820
 Seq. ID LIB3431-037-P1-N1-D3
 Method BLASTN
 NCBI GI g342643
 BLAST score 34
 E value 2.0e-09
 Match length 106
 % identity 83
 NCBI Description Maize mitochondrion with chloroplast insert containing rRNAs

Seq. No. 400821
 Seq. ID LIB3431-037-P1-N1-D8
 Method BLASTX
 NCBI GI g2501190
 BLAST score 202
 E value 1.0e-15
 Match length 60
 % identity 72
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
 >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 400822
 Seq. ID LIB3431-037-P1-N1-E11
 Method BLASTX
 NCBI GI g132105
 BLAST score 443
 E value 7.0e-44
 Match length 80
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_



```
Seq. No.      400833
Seq. ID      LIB3431-037-P1-N1-F4
Method       BLASTX
NCBI GI      g128690
BLAST score   533
E value      2.0e-54
Match length  120
% identity    88
NCBI Description  NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
>gi_66161_pir_DERZN3 NADH dehydrogenase (ubiquinone) (EC
1.6.5.3) chain 3 - rice chloroplast >gi_11989_emb_CAA34001_
(X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa]
>gi_226610_prf_1603356AG NADH dehydrogenase ND3 [Oryza
sativa]
```

```
Seq. No.          400834
Seq. ID           LIB3431-037-P1-N1-F5
Method            BLASTX
NCBI GI           g1311176
BLAST score       333
E value           6.0e-31
Match length      65
% identity        97
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
                  (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                  >gi_72683_pir_F1BH4 photosystem I chain IV precursor -
                  barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
                  -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A
                  10.8kd photosystem I protein [Hordeum vulgare var.
                  distichum]
```

```
Seq. No.          400835
Seq. ID          LIB3431-037-P1-N1-F6
Method          BLASTX
NCBI GI         g548605
BLAST score      277
E value         2.0e-24
Match length     59
% identity       90
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir_A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
```

```
Seq. No.      400836
Seq. ID      LIB3431-037-P1-N1-F8
Method       BLASTX
NCBI GI      g2072555
BLAST score   237
E value      1.0e-19
Match length  44
% identity    100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
```


[illegible]

Seq. No.	400838
Seq. ID	LIB3431-037-P1-N1-G1
Method	BLASTN
NCBI GI	g2950394
BLAST score	35
E value	5.0e-10
Match length	51
% identity	92
NCBI Description	Zea mays me gene, exons 1 to

```
Seq. No.      400840
Seq. ID      LIB3431-037-P1-N1-G12
Method       BLASTN
NCBI GI      g2072554
BLAST score   220
E value      1.0e-120
Match length  243
% identity    98
NCBI Description  Oryza sativa metallothionein-like protein mRNA, complete
                  cds
```

51364

[illegible]

```
Seq. No.      400863
Seq. ID      LIB3431-038-P1-K1-A3
Method       BLASTX
NCBI GI      g3548808
BLAST score   322
E value      8.0e-30
Match length  81
% identity    67
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
```

Seq. No.	400864
Seq. ID	LIB3431-038-P1-K1-A4
Method	BLASTX
NCBI GI	g5031281
BLAST score	274
E value	4.0e-24
Match length	71
% identity	75
NCBI Description	(AF139499) unknown [Prunus armeniaca]

```
Seq. No.      400865
Seq. ID      LIB3431-038-P1-K1-A5
Method       BLASTX
NCBI GI      g2293480
BLAST score   431
E value      2.0e-42
Match length  85
% identity    98
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
```

```
Seq. No.      400866
Seq. ID      LIB3431-038-P1-K1-A7
Method       BLASTX
NCBI GI      g282882
BLAST score   175
E value      2.0e-12
Match length  105
% identity    37
NCBI Description  receptor-like protein kinase precursor - Arabidopsis
                  thaliana >gi_166848 (M84659) receptor-like protein kinase
                  [Arabidopsis thaliana]
```

51369

% identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 400878
 Seq. ID LIB3431-038-P1-K1-C10
 Method BLASTX
 NCBI GI g167097
 BLAST score 188
 E value 9.0e-27
 Match length 76
 % identity 82
 NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase
 [Hordeum vulgare]

Seq. No. 400879
 Seq. ID LIB3431-038-P1-K1-C11
 Method BLASTX
 NCBI GI g4204263
 BLAST score 349
 E value 6.0e-33
 Match length 113
 % identity 60
 NCBI Description (AC005223) 40409 [Arabidopsis thaliana]

Seq. No. 400880
 Seq. ID LIB3431-038-P1-K1-C12
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 8.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 400881
 Seq. ID LIB3431-038-P1-K1-C2
 Method BLASTX
 NCBI GI g320618
 BLAST score 333
 E value 4.0e-31
 Match length 92
 % identity 74
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

[illegible]

```
Seq. No.      400903
Seq. ID      LIB3431-038-P1-K1-F1
Method       BLASTX
NCBI GI      g132105
BLAST score   591
E value      3.0e-61
Match length  127
% identity    87
NCBI Description  RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose bisphtosphate
                carboxylase S [Oryza sativa]
```

Seq. No.	400904
Seq. ID	LIB3431-038-P1-K1-F10
Method	BLASTX
NCBI GI	g224293
BLAST score	409
E value	6.0e-40
Match length	82
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

```
Seq. No.      400905
Seq. ID      LIB3431-038-P1-K1-F11
Method       BLASTX
NCBI GI      g132105
BLAST score   322
E value      4.0e-46
Match length  110
% identity    87
NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```


sativa] >gi_226375_prf_1508256A ribulose biphosphate
carboxylase S [Oryza sativa]

Seq. No. 400906
Seq. ID LIB3431-038-P1-K1-F2
Method BLASTN
NCBI GI g6015437
BLAST score 35
E value 5.0e-10
Match length 35
% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 400907
Seq. ID LIB3431-038-P1-K1-F3
Method BLASTX
NCBI GI g2497903
BLAST score 220
E value 8.0e-18
Match length 59
% identity 68
NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2
>gi_1752831_dbj_BAA14038.1_ (D89931) metallothionein-like
protein [Oryza sativa] >gi_1815628 (U43530)
metallothionein-like type 2 [Oryza sativa]

Seq. No. 400908
Seq. ID LIB3431-038-P1-K1-F4
Method BLASTX
NCBI GI g3928097
BLAST score 213
E value 6.0e-17
Match length 94
% identity 47
NCBI Description (AC005770) unknown protein, 5' partial [Arabidopsis
thaliana]

Seq. No. 400909
Seq. ID LIB3431-038-P1-K1-F5
Method BLASTX
NCBI GI g2407281
BLAST score 653
E value 1.0e-68
Match length 127
% identity 94
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
subunit [Oryza sativa]

Seq. No. 400910
Seq. ID LIB3431-038-P1-K1-F6
Method BLASTX
NCBI GI g548603
BLAST score 407
E value 1.0e-39
Match length 118
% identity 71
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR


```
>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
synthetase [Oryza sativa]
```

```
Seq. No.          400979
Seq. ID          LIB3431-038-P1-N1-H12
Method          BLASTX
NCBI GI         g5174741
BLAST score      165
E value         2.0e-11
Match length     64
% identity       52
NCBI Description  ubiquitin carboxyl-terminal esterase L3 (ubiquitin
                  thiolesterase) >gi_136682_sp_P15374_UBL3_HUMAN UBIQUITIN
                  CARBOXYL-TERMINAL HYDROLASE ISOZYME L3 (UCH-L3) (UBIQUITIN
                  THIOLESTERASE L3) >gi_108014_pir_A40085 ubiquitin
                  carboxyl-terminal proteinase (EC 3.4.-.-) L3 - human
                  >gi_2914274_pdb_1UCH_ Deubiquitinating Enzyme Uch-L3
                  (Human) At 1.8 Angstrom Resolution >gi_340074 (M30496)
                  ubiquitin carboxyl-terminal hydrolase [Homo sapiens]
```

```
Seq. No.      400980
Seq. ID      LIB3431-038-P1-N1-H3
Method       BLASTX
NCBI GI      g5381319
BLAST score   271
E value      9.0e-24
Match length  55
% identity    95
NCBI Description (AF091621) ubiquitin-conjugating enzyme E2 [Catharanthus roseus]
```

Seq. No.	400981
Seq. ID	LIB3431-038-P1-N1-H4
Method	BLASTX
NCBI GI	g289920
BLAST score	291
E value	4.0e-26
Match length	55
% identity	100
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	400982
Seq. ID	LIB3431-038-P1-N1-H6
Method	BLASTN
NCBI GI	g3063523
BLAST score	58
E value	9.0e-24
Match length	146
% identity	85
NCBI Description	Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds

```
Seq. No.      400983
Seq. ID      LIB3431-038-P1-N1-H8
Method       BLASTX
NCBI GI      q5007084
```


Seq. No.	400989
Seq. ID	LIB3431-039-P1-K2-B10
Method	BLASTN
NCBI GI	g11957
BLAST score	378
E value	0.0e+00
Match length	411
% identity	98
NCBI Description	Rice complete chloroplast genome

Seq. No.	400990
Seq. ID	LIB3431-039-P1-K2-B11
Method	BLASTN
NCBI GI	g11957
BLAST score	127
E value	4.0e-65
Match length	251
% identity	88
NCBI Description	Rice complete chloroplast genome

```
Seq. No.      400991
Seq. ID      LIB3431-039-P1-K2-B2
Method       BLASTX
NCBI GI      g115772
BLAST score   189
E value      1.0e-25
Match length  62
% identity    94
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
                  CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding
                  protein 1R precursor - rice >gi_20178_emb_CAA32108_
                  (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                  [Oryza sativa]
```

```
Seq. No.      400992
Seq. ID      LIB3431-039-P1-K2-B3
Method       BLASTX
NCBI GI      g733454
BLAST score   483
E value      9.0e-49
Match length  111
% identity    82
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
               [Zea mays]
```

```
Seq. No.          400993
Seq. ID           LIB3431-039-P1-K2-B6
Method            BLASTX
NCBI GI           g3126854
BLAST score       149
E value           7.0e-10
Match length      30
% identity        100
NCBI Description  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```


Match length 66
 % identity 74
 NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
 (AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein -
 rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
 sativa]

Seq. No. 401024
 Seq. ID LIB3431-039-P1-K2-G3
 Method BLASTX
 NCBI GI g2462762
 BLAST score 337
 E value 3.0e-39
 Match length 121
 % identity 69
 NCBI Description (AC002292) Highly similar to auxin-induced protein
 (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 401025
 Seq. ID LIB3431-039-P1-K2-G4
 Method BLASTX
 NCBI GI g3063524
 BLAST score 184
 E value 3.0e-14
 Match length 51
 % identity 75
 NCBI Description (AF052305) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

Seq. No. 401026
 Seq. ID LIB3431-039-P1-K2-G5
 Method BLASTX
 NCBI GI g82080
 BLAST score 364
 E value 9.0e-35
 Match length 113
 % identity 64
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 401027
 Seq. ID LIB3431-039-P1-K2-G6
 Method BLASTX
 NCBI GI g320618
 BLAST score 199
 E value 9.0e-16
 Match length 57
 % identity 72
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 401028
 Seq. ID LIB3431-039-P1-K2-G8


```
E value      1.0e-87
Match length 253
% identity   91
NCBI Description Oryza sativa mRNA for the small subunit of
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
pOSSS1139
```

```
Seq. No.      401098
Seq. ID      LIB3431-040-P1-K2-C3
Method       BLASTX
NCBI GI      g2130042
BLAST score   486
E value      6.0e-56
Match length  126
% identity    92
NCBI Description  Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916)
                protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
                vulgare]
```

Seq. No.	401099
Seq. ID	LIB3431-040-P1-K2-C4
Method	BLASTN
NCBI GI	g5295936
BLAST score	36
E value	3.0e-11
Match length	48
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

```
Seq. No.      401100
Seq. ID       LIB3431-040-P1-K2-C5
Method        BLASTX
NCBI GI       g3559814
BLAST score   658
E value       4.0e-69
Match length  146
% identity    86
NCBI Description (Y15781) transketolase 1 [Capsicum annuum]
```

```
Seq. No.          401101
Seq. ID           LIB3431-040-P1-K2-C6
Method            BLASTX
NCBI GI           g2501356
BLAST score       523
E value           3.0e-53
Match length      139
% identity        74
NCBI Description   TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)
                  >gi_1658322_emb_CAA90427_ (Z50099) transketolase precursor
                  [Solanum tuberosum]
```

Seq. No.	401102
Seq. ID	LIB3431-040-P1-K2-C7
Method	BLASTX
NCBI GI	g4995921
BLAST score	230

% identity	84
NCBI Description	(AF022740) glycolate oxidase [Oryza sativa]
Seq. No.	401127
Seq. ID	LIB3431-040-P1-K2-G2
Method	BLASTX
NCBI GI	g3914603
BLAST score	707
E value	7.0e-75
Match length	146
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]
Seq. No.	401128
Seq. ID	LIB3431-040-P1-K2-G3
Method	BLASTN
NCBI GI	g2072554
BLAST score	214
E value	1.0e-117
Match length	309
% identity	92
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds
Seq. No.	401129
Seq. ID	LIB3431-040-P1-K2-G4
Method	BLASTX
NCBI GI	g461498
BLAST score	248
E value	2.0e-21
Match length	84
% identity	55
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir_S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]
Seq. No.	401130
Seq. ID	LIB3431-040-P1-K2-G5
Method	BLASTX
NCBI GI	g4138290
BLAST score	360
E value	7.0e-35
Match length	95
% identity	75
NCBI Description	(AJ005841) thioredoxin M [Oryza sativa]
Seq. No.	401131
Seq. ID	LIB3431-040-P1-K2-G7
Method	BLASTX
NCBI GI	g3080420
BLAST score	392
E value	6.0e-38

Match length	142
% identity	56
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	401132
Seq. ID	LIB3431-040-P1-K2-G8
Method	BLASTX
NCBI GI	g3080420
BLAST score	389
E value	1.0e-37
Match length	120
% identity	62
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	401133
Seq. ID	LIB3431-040-P1-K2-H10
Method	BLASTN
NCBI GI	g6103440
BLAST score	93
E value	5.0e-45
Match length	149
% identity	91
NCBI Description	Oryza sativa metallothionein-like protein (ML2) mRNA, complete cds

Seq. No.	401134
Seq. ID	LIB3431-040-P1-K2-H12
Method	BLASTN
NCBI GI	g2072554
BLAST score	146
E value	3.0e-76
Match length	186
% identity	95
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	401135
Seq. ID	LIB3431-040-P1-K2-H2
Method	BLASTN
NCBI GI	g3135542
BLAST score	39
E value	8.0e-13
Match length	67
% identity	90
NCBI Description	Oryza sativa aquaporin (PIP2a) mRNA, complete cds

```
Seq. No.      401136
Seq. ID      LIB3431-040-P1-K2-H5
Method       BLASTX
NCBI GI      g4584342
BLAST score   221
E value      6.0e-18
Match length  120
% identity    42
NCBI Description (AC007127) putative ubiquitin protein [Arabidopsis
```


09634016-101000

Match length 67
% identity 97
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401171
Seq. ID LIB3431-040-P1-N1-H7
Method BLASTX
NCBI GI g347451
BLAST score 376
E value 4.0e-36
Match length 69
% identity 99
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 401172
Seq. ID LIB3431-040-P1-N1-H9
Method BLASTN
NCBI GI g218209
BLAST score 149
E value 5.0e-78
Match length 329
% identity 96
NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 401173
Seq. ID LIB3431-041-P1-N1-A10
Method BLASTN
NCBI GI g3126853
BLAST score 230
E value 1.0e-126
Match length 249
% identity 99
NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 401174
Seq. ID LIB3431-041-P1-N1-A2
Method BLASTX
NCBI GI g115787
BLAST score 432
E value 1.0e-42
Match length 82
% identity 100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401175
Seq. ID LIB3431-041-P1-N1-A3
Method BLASTX
NCBI GI g4079798


```
BLAST score      277
E value         2.0e-24
Match length    52
% identity      100
NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza
sativa]
```

Seq. No.	401176
Seq. ID	LIB3431-041-P1-N1-A4
Method	BLASTX
NCBI GI	g2982301
BLAST score	255
E value	8.0e-22
Match length	91
% identity	55
NCBI Description	(AF051235) YGL010w-like protein [Picea mariana]

```
Seq. No.          401177
Seq. ID           LIB3431-041-P1-N1-A6
Method            BLASTX
NCBI GI           g6093827
BLAST score       169
E. value          1.0e-11
Match length      97
% identity        41
NCBI Description   PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
                  [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
                  PROTEIN PSBY-2] >gi_2956690_emb_CAA11248 (AJ223306) PSBY
                  [Arabidopsis thaliana] >gi_3414928 (AF079800) Psby
                  precursor [Arabidopsis thaliana]
```

```
Seq. No.          401178
Seq. ID           LIB3431-041-P1-N1-A7
Method            BLASTX
NCBI GI           g120661
BLAST score       225
E value           2.0e-18
Match length      43
% identity        95
NCBI Description   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
                   PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
                   dehydrogenase A-subunit precursor [Nicotiana tabacum]
```

Seq. No.	401179
Seq. ID	LIB3431-041-P1-N1-A9
Method	BLASTN
NCBI GI	g11640
BLAST score	45
E value	4.0e-16
Match length	137
% identity	42
NCBI Description	Liverwort Marchantia polymorpha chloroplast genome DNA

```
Seq. No.      401180
Seq. ID      LIB3431-041-P1-N1-B1
Method       BLASTN
NCBI GI      q2072554
```



```
E value          4.0e-24
Match length     79
% identity       71
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
light-regulated gene [Oryza sativa]
```

Seq. No.	401186
Seq. ID	LIB3431-041-P1-N1-B8
Method	BLASTX
NCBI GI	g2997591
BLAST score	238
E value	6.0e-20
Match length	61
% identity	79
NCBI Description	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]

```
Seq. No.          401187
Seq. ID           LIB3431-041-P1-N1-C1
Method            BLASTX
NCBI GI           g131225
BLAST score       216
E value           2.0e-17
Match length      56
% identity        73
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
```

Seq. No.	401188
Seq. ID	LIB3431-041-P1-N1-C10
Method	BLASTX
NCBI GI	g131225
BLAST score	327
E value	3.0e-30
Match length	92
% identity	70
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	401189
Seq. ID	LIB3431-041-P1-N1-C11
Method	BLASTN
NCBI GI	g20262
BLAST score	265
E value	1.0e-147
Match length	272
% identity	99
NCBI Description	O.sativa light-induced mRNA

Seq. No.	401190
Seq. ID	LIB3431-041-P1-N1-C12
Method	BLASTX

NCBI GI	g2570511
BLAST score	163
E value	2.0e-26
Match length	74
% identity	80
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

```
Seq. No.      401191
Seq. ID      LIB3431-041-P1-N1-C5
Method       BLASTX
NCBI GI      g6015059
BLAST score   422
E value      2.0e-41
Match length  83
% identity    100
NCBI Description  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096
                (AF030517) translation elongation factor-1 alpha; EF-1
                alpha [Oryza sativa]
```

```
Seq. No.      401192
Seq. ID      LIB3431-041-P1-N1-C8
Method       BLASTX
NCBI GI      g730510
BLAST score   150
E value      1.0e-09
Match length  45
% identity    67
NCBI Description  RAS-RELATED PROTEIN RIC1 >gi_542150_pir_S38740 GTP-binding
protein - rice >gi_432607_gb_AAB28535_ (S66160) ras-related
GTP binding protein possessing GTPase activity=ric1 [Oryza
sativa=rice, var. Yamahoushi, callus, Peptide, 202 aa]
[Oryza sativa]
```

Seq. No.	401193
Seq. ID	LIB3431-041-P1-N1-D2
Method	BLASTN
NCBI GI	g6006355
BLAST score	88
E value	1.0e-41
Match length	130
% identity	46
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

```
Seq. No.          401194
Seq. ID           LIB3431-041-P1-N1-D3
Method            BLASTX
NCBI GI           g4877984
BLAST score       262
E value           1.0e-22
Match length      53
% identity        96
NCBI Description   (AF145755) THA4 [Zea mays]
```

```
Seq. No.      401195
Seq. ID      LIB3431-041-P1-N1-D7
Method       BLASTN
NCBI GI      q218154
```


BLAST score 46
 E value 1.0e-16
 Match length 46
 % identity 100
 NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,
 clone:Aldp

Seq. No. 401196
 Seq. ID LIB3431-041-P1-N1-E10
 Method BLASTX
 NCBI GI g3582335
 BLAST score 493
 E value 1.0e-49
 Match length 105
 % identity 84
 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 401197
 Seq. ID LIB3431-041-P1-N1-E11
 Method BLASTX
 NCBI GI g3738261
 BLAST score 171
 E value 3.0e-12
 Match length 58
 % identity 67
 NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus
 nigra]

Seq. No. 401198
 Seq. ID LIB3431-041-P1-N1-E5
 Method BLASTN
 NCBI GI g416266
 BLAST score 44
 E value 2.0e-15
 Match length 126
 % identity 83
 NCBI Description Rice mRNA for oxygen-evolving protein, partial sequence

Seq. No. 401199
 Seq. ID LIB3431-041-P1-N1-E6
 Method BLASTN
 NCBI GI g3075487
 BLAST score 308
 E value 1.0e-173
 Match length 315
 % identity 99
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
 mRNA, complete cds

Seq. No. 401200
 Seq. ID LIB3431-041-P1-N1-E7
 Method BLASTN
 NCBI GI g3885887
 BLAST score 465
 E value 0.0e+00
 Match length 465
 % identity 100


```
Seq. No.          401216
Seq. ID          LIB3431-041-P1-N1-H8
Method           BLASTX
NCBI GI          g3126854
BLAST score      235
E value          1.0e-19
Match length     55
% identity       84
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.      401217
Seq. ID      LIB3431-041-P2-K1-A2
Method       BLASTX
NCBI GI      g320618
BLAST score   380
E value      3.0e-59
Match length  135
% identity    87
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
                >gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
                chlorophyll a/b-binding protein [Oryza sativa]
                >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
                [Oryza sativa]
```

```
Seq. No.          401218
Seq. ID           LIB3431-041-P2-K1-A3
Method            BLASTX
NCBI GI           g4079798
BLAST score       218
E value           3.0e-18
Match length      50
% identity         90
NCBI Description   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                   sativa]
```

```
Seq. No.      401219
Seq. ID      LIB3431-041-P2-K1-A7
Method       BLASTX
NCBI GI      g120657
BLAST score   575
E value      2.0e-59
Match length  136
% identity    85
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                  CHLOROPLAST >gi_66024_pir_DEZMG3
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  maize >gi_168479 (M18976) glyceraldehyde-3-phosphate
                  dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408)
                  glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
```

```
Seq. No.      401220
Seq. ID      LIB3431-041-P2-K1-B1
Method       BLASTN
NCBI GI      g6103440
BLAST score  313
```


E value	1.0e-176
Match length	332
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein (ML2) mRNA, complete cds
Seq. No.	401221
Seq. ID	LIB3431-041-P2-K1-B10
Method	BLASTX
NCBI GI	g1835731
BLAST score	297
E value	4.0e-31
Match length	90
% identity	80
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.	401222
Seq. ID	LIB3431-041-P2-K1-B11
Method	BLASTX
NCBI GI	g4958922
BLAST score	219
E value	1.0e-17
Match length	88
% identity	53
NCBI Description	(AB027757) NADPH oxidoreductase homolog [Cicer arietinum]
Seq. No.	401223
Seq. ID	LIB3431-041-P2-K1-B12
Method	BLASTX
NCBI GI	g6094430
BLAST score	200
E value	6.0e-16
Match length	70
% identity	60
NCBI Description	TUBULIN ALPHA-2 CHAIN (ALPHA-TUBULIN 2) >gi_2511533 (AF008121) alpha-tubulin 2 [Eleusine indica]
Seq. No.	401224
Seq. ID	LIB3431-041-P2-K1-B6
Method	BLASTX
NCBI GI	g2570511
BLAST score	494
E value	5.0e-50
Match length	95
% identity	98
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.	401225
Seq. ID	LIB3431-041-P2-K1-B7
Method	BLASTN
NCBI GI	g20262
BLAST score	296
E value	1.0e-166
Match length	328
% identity	98
NCBI Description	O.sativa light-induced mRNA

NCBI GI	g3551954
BLAST score	349
E value	9.0e-33
Match length	137
% identity	51
NCBI Description	(AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

```
Seq. No.      401232
Seq. ID      LIB3431-041-P2-K1-C8
Method       BLASTN
NCBI GI      g432606
BLAST score   75
E value      4.0e-34
Match length  154
% identity    99
NCBI Description  ric1=ras-related GTP binding protein possessing GTPase
activity [Oryza sativa=rice, Yamahoushi, callus, mRNA, 955
nt]
```

[illegible]

Seq. No.	401234
Seq. ID	LIB3431-041-P2-K1-D2
Method	BLASTN
NCBI GI	g6006355
BLAST score	132
E value	6.0e-68
Match length	197
% identity	46
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

```
Seq. No.          401235
Seq. ID           LIB3431-041-P2-K1-D3
Method            BLASTX
NCBI GI           g4877984
BLAST score       369
E value           3.0e-35
Match length      143
% identity        57
NCBI Description  (AF145755) THA4 [Zea mays]
```

Seq. No.	401236
Seq. ID	LIB3431-041-P2-K1-D6


```
Seq. ID      LIB3431-041-P2-K1-E2
Method       BLASTN
NCBI GI      g6015437
BLAST score   36
E value      3.0e-11
Match length  36
% identity    100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
```

```
Seq. No.          401242
Seq. ID           LIB3431-041-P2-K1-E3
Method            BLASTX
NCBI GI           g3986695
BLAST score       519
E value           7.0e-53
Match length      122
% identity        86
NCBI Description   (AF101423) ribosomal protein L12 [Cichorium intybus]
```

```
Seq. No.      401243
Seq. ID      LIB3431-041-P2-K1-E5
Method       BLASTX
NCBI GI      g131388
BLAST score   188
E value      4.0e-14
Match length  87
% identity    56
NCBI Description  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260
photosystem II oxygen-evolving complex protein 1 - common
wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
33kDa oxygen evolving protein of photosystem II [Triticum
aestivum]
```

```
Seq. No.          401244
Seq. ID           LIB3431-041-P2-K1-E6
Method            BLASTX
NCBI GI           g3075488
BLAST score       426
E value           2.0e-51
Match length      126
% identity        84
NCBI Description  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
```

```
Seq. No.      401245
Seq. ID       LIB3431-041-P2-K1-E7
Method        BLASTN
NCBI GI       g3885887
BLAST score    355
E value       0.0e+00
Match length   363
% identity     100
NCBI Description  Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
```

Seq. No. 401246


```
Seq. ID      LIB3431-041-P2-K1-E8
Method       BLASTX
NCBI GI      g3386621
BLAST score   511
E value      7.0e-52
Match length  117
% identity    85
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      401247
Seq. ID      LIB3431-041-P2-K1-E9
Method       BLASTX
NCBI GI      g3980400
BLAST score   487
E value      5.0e-49
Match length  166
% identity    58
NCBI Description (AC004561) putative tropinone reductase [Arabidopsis thaliana]
```

```
Seq. No.          401248
Seq. ID           LIB3431-041-P2-K1-F1
Method            BLASTX
NCBI GI           g3377797
BLAST score       295
E value           1.0e-26
Match length      116
% identity        53
NCBI Description   (AF075597) Similar to 60S ribosome protein L19; coded for
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
```

Seq. No.	401249
Seq. ID	LIB3431-041-P2-K1-F11
Method	BLASTN
NCBI GI	g2072554
BLAST score	307
E value	1.0e-172
Match length	319
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	401250
Seq. ID	LIB3431-041-P2-K1-F12
Method	BLASTX
NCBI GI	g1835731
BLAST score	537
E value	7.0e-55
Match length	114
% identity	90
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401251
Seq. ID LIB3431-041-P2-K1-F2

[illegible]

E value	3.0e-31
Match length	111
% identity	62
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	401291
Seq. ID	LIB3431-042-P1-K1-C9
Method	BLASTX
NCBI GI	g2911068
BLAST score	199
E value	2.0e-15
Match length	43
% identity	79
NCBI Description	(AL021960) G10-like protein [Arabidopsis thaliana]

Seq. No.	401292
Seq. ID	LIB3431-042-P1-K1-D12
Method	BLASTX
NCBI GI	g322867
BLAST score	520
E value	5.0e-53
Match length	135
% identity	75
NCBI Description	translation initiation factor eIF-4F isozyme form subunit p82 - wheat

```
Seq. No.      401293
Seq. ID      LIB3431-042-P1-K1-D3
Method       BLASTX
NCBI GI      g3914603
BLAST score   287
E value      1.0e-25
Match length  134
% identity    51
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                activase [Oryza sativa]
```

```
Seq. No.          401294
Seq. ID           LIB3431-042-P1-K1-D4
Method            BLASTX
NCBI GI           g733454
BLAST score       503
E value           6.0e-51
Match length      118
% identity        81
NCBI Description  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                  [Zea mays]
```

Seq. No.	401295
Seq. ID	LIB3431-042-P1-K1-D6
Method	BLASTX
NCBI GI	g3913018
BLAST score	740
E value	9.0e-79

NCBI GI	g3789954
BLAST score	667
E value	3.0e-70
Match length	124
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	401315
Seq. ID	LIB3431-042-P1-K1-G11
Method	BLASTN
NCBI GI	g5803242
BLAST score	86
E value	2.0e-40
Match length	157
% identity	20
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

```
Seq. No.      401316
Seq. ID      LIB3431-042-P1-K1-G12
Method       BLASTX
NCBI GI      g1173347
BLAST score   711
E value      2.0e-75
Match length  141
% identity    94
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
                3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                aestivum]
```

```
Seq. No.      401317
Seq. ID       LIB3431-042-P1-K1-G2
Method        BLASTX
NCBI GI       gi1708424
BLAST score    408
E value       8.0e-40
Match length   112
% identity     65
NCBI Description  ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590)
                isoflavone reductase-like protein [Lupinus albus]
```

Seq. No.	401318
Seq. ID	LIB3431-042-P1-K1-G3
Method	BLASTN
NCBI GI	g1658312
BLAST score	104
E value	3.0e-51
Match length	104
% identity	50
NCBI Description	O.sativa osr40q2 gene

Seq. No.	401319
Seq. ID	LIB3431-042-P1-K1-G4
Method	BLASTX

[illegible]

```
Seq. No.      401325
Seq. ID      LIB3431-042-P1-K1-H10
Method       BLASTX
NCBI GI      g3789954
BLAST score   615
E value      4.0e-64
Match length  115
% identity    99
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]
```

```
Seq. No.          401327
Seq. ID           LIB3431-042-P1-K1-H2
Method            BLASTX
NCBI GI           g6093778
BLAST score       370
E value           2.0e-35
Match length      103
% identity        75
NCBI Description  PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3)
                  (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3)
                  >gi_2511574_emb_CAA73619.1_(Y13176) multicatalytic
                  endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520)
                  20S proteasome subunit PAB1 [Arabidopsis thaliana]
                  >gi_4966368_gb_AAD34699.1_AC006341.27 (AC006341) Identical
                  to gb_Y13176 Arabidopsis thaliana mRNA for proteasome
                  subunit prc3. ESTs gb H36972, gb T22551 and gb T13800 come
```


Variable	Mean	SD	Min	Max
Age	34.5	10.2	22	55
Gender	Male	100%		
Marital status	Married	100%		
Education	High school	100%		
Occupation	Teacher	100%		
Income	Low	100%		
Religion	Islam	100%		
Health status	Good	100%		
Smoking status	Non-smoker	100%		
Alcohol consumption	None	100%		
Exercise frequency	Low	100%		
Stress level	High	100%		
Sleep quality	Poor	100%		
Appetite	Low	100%		
Weight change	Decrease	100%		
Blood pressure	High	100%		
Cholesterol level	High	100%		
Glucose level	High	100%		
Hemoglobin level	Low	100%		
White blood cell count	High	100%		
Platelet count	Low	100%		
Red blood cell count	Low	100%		
Hematocrit	Low	100%		
Hemoglobin A1c	High	100%		
Triglyceride level	High	100%		
LDL cholesterol	High	100%		
HDL cholesterol	Low	100%		
Protein level	Low	100%		
Albumin level	Low	100%		
Bilirubin level	High	100%		
Aspartate aminotransferase	High	100%		
Alanine aminotransferase	High	100%		
Gamma-glutamyl transferase	High	100%		
Creatinine level	High	100%		
BUN level	High	100%		
Urea level	High	100%		
Calcium level	Low	100%		
Phosphorus level	High	100%		
Potassium level	Low	100%		
Sodium level	High	100%		
Magnesium level	Low	100%		
Zinc level	Low	100%		
Copper level	Low	100%		
Manganese level	Low	100%		
Selenium level	Low	100%		
Iron level	Low	100%		
Vitamin A level	Low	100%		
Vitamin B1 level	Low	100%		
Vitamin B2 level	Low	100%		
Vitamin B3 level	Low	100%		
Vitamin B5 level	Low	100%		
Vitamin B6 level	Low	100%		
Vitamin B7 level	Low	100%		
Vitamin B9 level	Low	100%		
Vitamin B12 level	Low	100%		
Vitamin C level	Low	100%		
Vitamin D level	Low	100%		
Vitamin E level	Low	100%		
Vitamin K level	Low	100%		
Vitamin P level	Low	100%		
Vitamin Q level	Low	100%		
Vitamin R level	Low	100%		
Vitamin S level	Low	100%		
Vitamin T level	Low	100%		
Vitamin U level	Low	100%		
Vitamin V level	Low	100%		
Vitamin W level	Low	100%		
Vitamin X level	Low	100%		
Vitamin Y level	Low	100%		
Vitamin Z level	Low	100%		
Vitamin AA level	Low	100%		
Vitamin AB level	Low	100%		
Vitamin AC level	Low	100%		
Vitamin AD level	Low	100%		
Vitamin AE level	Low	100%		
Vitamin AF level	Low	100%		
Vitamin AG level	Low	100%		
Vitamin AH level	Low	100%		
Vitamin AI level	Low	100%		
Vitamin AJ level	Low	100%		
Vitamin AK level	Low	100%		
Vitamin AL level	Low	100%		
Vitamin AM level	Low	100%		
Vitamin AN level	Low	100%		
Vitamin AO level	Low	100%		
Vitamin AP level	Low	100%		
Vitamin AQ level	Low	100%		
Vitamin AR level	Low	100%		
Vitamin AS level	Low	100%		
Vitamin AT level	Low	100%		
Vitamin AU level	Low	100%		
Vitamin AV level	Low	100%		
Vitamin AW level	Low	100%		
Vitamin AX level	Low	100%		
Vitamin AY level	Low	100%		
Vitamin AZ level	Low	100%		

51464

Match length	87
% identity	86
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

```
Seq. No.      401348
Seq. ID      LIB3431-042-P1-N1-C11
Method       BLASTX
NCBI GI      g132105
BLAST score   421
E value      3.0e-41
Match length  76
% identity    100
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]
```

Seq. No.	401349
Seq. ID	LIB3431-042-P1-N1-C4
Method	BLASTX
NCBI GI	g1483563
BLAST score	265
E value	6.0e-23
Match length	53
% identity	92
NCBI Description	(X99825) leucine aminopeptidase [Petroselinum crispum]

```
Seq. No.          401350
Seq. ID           LIB3431-042-P1-N1-C5
Method            BLASTX
NCBI GI           g671740
BLAST score       227
E value           1.0e-18
Match length      56
% identity        79
NCBI Description   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
```

Seq. No.	401351
Seq. ID	LIB3431-042-P1-N1-C6
Method	BLASTN
NCBI GI	g454881
BLAST score	207
E value	1.0e-113
Match length	234
% identity	97
NCBI Description	Rice gene for thioredoxin h, complete cds

```
Seq. No.      401352
Seq. ID      LIB3431-042-P1-N1-C7
Method       BLASTX
```



```

NCBI GI          g417260
BLAST score      406
E value          2.0e-39
Match length     128
% identity       65
NCBI Description  LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
                  lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]

```

```
Seq. No.          401353
Seq. ID           LIB3431-042-P1-N1-C9
Method            BLASTN
NCBI GI           g4079797
BLAST score       66
E value           1.0e-28
Match length      246
% identity        81
NCBI Description   Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
                  complete cds
```

```
Seq. No.      401354
Seq. ID      LIB3431-042-P1-N1-D10
Method       BLASTX
NCBI GI      g132105
BLAST score   522
E value      4.0e-53
Match length  94
% identity    100
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                carboxylase S [Oryza sativa]
```

```
Seq. No.      401355
Seq. ID      LIB3431-042-P1-N1-D11
Method       BLASTX
NCBI GI      g115787
BLAST score   402
E value      5.0e-39
Match length  77
% identity    99
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

```
Seq. No.      401356
Seq. ID      LIB3431-042-P1-N1-D12
Method       BLASTN
NCBI GI      g452439
BLAST score  68
```



```
Seq. No.          401381
Seq. ID           LIB3431-042-P1-N1-G4
Method            BLASTX
NCBI GI           g132105
BLAST score       295
E value           1.0e-26
Match length      57
% identity        98
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. No.          401382
Seq. ID          LIB3431-042-P1-N1-G6
Method          BLASTX
NCBI GI         g3915088
BLAST score      254
E value         9.0e-22
Match length    75
% identity      63
NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
                  4-HYDROXYLASE) (CA4H) (C4H) (P450C4H) (CYTOCHROME P450 73)
                  >gi_903872 (L38898) trans-cinnamate 4-monooxygenase
                  [Petroselinum crispum]
```

```
Seq. No.      401383
Seq. ID      LIB3431-042-P1-N1-G8
Method       BLASTX
NCBI GI      g1617197
BLAST score   276
E value      3.0e-24
Match length  71
% identity    70
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
```

```
Seq. No.      401384
Seq. ID      LIB3431-042-P1-N1-G9
Method       BLASTX
NCBI GI      g1617197
BLAST score   189
E value      3.0e-14
Match length  39
% identity    90
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
```

```
Seq. No.      401385
Seq. ID      LIB3431-042-P1-N1-H1
Method       BLASTX
NCBI GI      g128191
BLAST score  343
```


BLAST score 366
 E value 5.0e-35
 Match length 67
 % identity 97
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
 (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
 subunit precursor [Zea mays]

Seq. No. 401391
 Seq. ID LIB3431-043-P1-K1-A1
 Method BLASTX
 NCBI GI g132105
 BLAST score 735
 E value 4.0e-78
 Match length 156
 % identity 90
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401392
 Seq. ID LIB3431-043-P1-K1-A11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 628
 E value 1.0e-65
 Match length 119
 % identity 99
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401393
 Seq. ID LIB3431-043-P1-K1-A12
 Method BLASTN
 NCBI GI g3885887
 BLAST score 112
 E value 2.0e-56
 Match length 143
 % identity 96
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
 complete cds

Seq. No. 401394
 Seq. ID LIB3431-043-P1-K1-A2
 Method BLASTX
 NCBI GI g3150410
 BLAST score 277
 E value 2.0e-24
 Match length 96
 % identity 60
 NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]


```

Seq. ID          LIB3431-043-P1-K1-B10
Method          BLASTX
NCBI GI         g132105
BLAST score      690
E value         8.0e-73
Match length     147
% identity       89
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose biphosphate
                carboxylase S [Oryza sativa]

```

```
Seq. No.      401401
Seq. ID      LIB3431-043-P1-K1-B11
Method       BLASTX
NCBI GI      g2499417
BLAST score   499
E value      2.0e-50
Match length  120
% identity    78
NCBI Description  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
                >gi_1085826_pir_S49248 H-protein - Flaveria anomala
                >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria
                anomala]
```

Seq. No.	401402
Seq. ID	LIB3431-043-P1-K1-B2
Method	BLASTX
NCBI GI	g4079798
BLAST score	537
E value	7.0e-55
Match length	104
% identity	100
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

```
Seq. No.      401403
Seq. ID      LIB3431-043-P1-K1-B3
Method       BLASTX
NCBI GI      g132105
BLAST score   584
E value      2.0e-60
Match length  110
% identity    97
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375 prf_1508256A ribulose bisphosphate
```



```
Match length      32
% identity        100
NCBI Description  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
```

```
Seq. No.      401413
Seq. ID      LIB3431-043-P1-K1-C5
Method       BLASTX
NCBI GI      g676884
BLAST score   289
E value      9.0e-26
Match length  77
% identity    71
NCBI Description (D29681) The expression is induced by Pi starvation.
[Nicotiana tabacum] >gi_1094819_prf__2106387C Al-induced
protein [Nicotiana tabacum]
```

Seq. No.	401414
Seq. ID	LIB3431-043-P1-K1-C6
Method	BLASTN
NCBI GI	g1661159
BLAST score	81
E value	5.0e-38
Match length	85
% identity	99
NCBI Description	Oryza sativa chlorophyll a/b binding protein (kod1895) mRNA, complete cds

```
Seq. No.          401415
Seq. ID          LIB3431-043-P1-K1-C7
Method           BLASTX
NCBI GI          g1835731
BLAST score      507
E value          2.0e-51
Match length     123
% identity       81
NCBI Description  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

```
Seq. No.      401416
Seq. ID      LIB3431-043-P1-K1-C9
Method       BLASTX
NCBI GI      g4587556
BLAST score   433
E value      1.0e-42
Match length  140
% identity    61
NCBI Description (AC006577) Similar to gi_1653162 (p)ppGpp
3-pyrophosphohydrolase from Synechocystis sp genome
gb_D90911. EST gb_W43807 comes from this gene.
[Arabidopsis thaliana]
```

```
Seq. No.      401417
Seq. ID      LIB3431-043-P1-K1-D1
Method       BLASTX
NCBI GI      g2618686
BLAST score  402
```


Method	BLASTX
NCBI GI	g417260
BLAST score	407
E value	1.0e-39
Match length	128
% identity	65
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]
Seq. No.	401423
Seq. ID	LIB3431-043-P1-K1-D7
Method	BLASTX
NCBI GI	g320618
BLAST score	530
E value	4.0e-54
Match length	121
% identity	83
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]
Seq. No.	401424
Seq. ID	LIB3431-043-P1-K1-D8
Method	BLASTX
NCBI GI	g4583548
BLAST score	723
E value	1.0e-76
Match length	183
% identity	78
NCBI Description	(AJ010820) chloroplast FtsY homolog [Arabidopsis thaliana]
Seq. No.	401425
Seq. ID	LIB3431-043-P1-K1-D9
Method	BLASTX
NCBI GI	g1749676
BLAST score	147
E value	3.0e-09
Match length	82
% identity	44
NCBI Description	(D89234) similar to Saccharomyces cerevisiae ORF YGR205W, EMBL Accession Number Z72990 [Schizosaccharomyces pombe]
Seq. No.	401426
Seq. ID	LIB3431-043-P1-K1-E1
Method	BLASTN
NCBI GI	g2773153
BLAST score	489
E value	0.0e+00
Match length	496
% identity	100
NCBI Description	Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds
Seq. No.	401427

BLAST score 339
 E value 9.0e-32
 Match length 66
 % identity 98
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401457
 Seq. ID LIB3431-043-P1-N1-B10
 Method BLASTX
 NCBI GI g132105
 BLAST score 508
 E value 1.0e-51
 Match length 91
 % identity 100
 NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401458
 Seq. ID LIB3431-043-P1-N1-B11
 Method BLASTX
 NCBI GI g2499417
 BLAST score 309
 E value 3.0e-28
 Match length 71
 % identity 82
 NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1085826_pir_S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No. 401459
 Seq. ID LIB3431-043-P1-N1-B2
 Method BLASTX
 NCBI GI g4079798
 BLAST score 183
 E value 2.0e-13
 Match length 34
 % identity 100
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401460
 Seq. ID LIB3431-043-P1-N1-B3
 Method BLASTX
 NCBI GI g347451
 BLAST score 248
 E value 4.0e-21
 Match length 48
 % identity 100

precursor - barley >gi_167087 (M61146) photosystem I
hydrophobic protein [Hordeum vulgare]

Seq. No. 401531
Seq. ID LIB3431-044-P1-K1-E5
Method BLASTX
NCBI GI g115787
BLAST score 762
E value 3.0e-81
Match length 149
% identity 99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 401532
Seq. ID LIB3431-044-P1-K1-E6
Method BLASTX
NCBI GI g5042409
BLAST score 442
E value 1.0e-43
Match length 136
% identity 64
NCBI Description (AC006193) Putative membrane related protein [Arabidopsis
thaliana]

Seq. No. 401533
Seq. ID LIB3431-044-P1-K1-E7
Method BLASTX
NCBI GI g5702231
BLAST score 190
E value 3.0e-14
Match length 108
% identity 44
NCBI Description (AF145386) hypersensitive reaction associated Ca²⁺-binding
protein [Phaseolus vulgaris]

Seq. No. 401534
Seq. ID LIB3431-044-P1-K1-E8
Method BLASTX
NCBI GI g548605
BLAST score 590
E value 5.0e-61
Match length 130
% identity 90
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
>gi_539055_pir_A48527 photosystem I protein psaK precursor
- barley >gi_304220 (L12707) photosystem I PSI-K subunit
[Hordeum vulgare]

Seq. No. 401535
Seq. ID LIB3431-044-P1-K1-E9
Method BLASTN
NCBI GI g3821780

indica]

Seq. No. 401600
Seq. ID LIB3431-045-P1-K1-A10
Method BLASTN
NCBI GI g5441876
BLAST score 106
E value 2.0e-52
Match length 327
% identity 35
NCBI Description Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
(contig b)

Seq. No. 401601
Seq. ID LIB3431-045-P1-K1-A12
Method BLASTX
NCBI GI g4689380
BLAST score 640
E value 5.0e-67
Match length 139
% identity 83
NCBI Description (AF139465) LHCI type III chlorophyll a/b binding protein
[Vigna radiata]

Seq. No. 401602
Seq. ID LIB3431-045-P1-K1-A3
Method BLASTX
NCBI GI g132105
BLAST score 752
E value 4.0e-80
Match length 160
% identity 90
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 401603
Seq. ID LIB3431-045-P1-K1-A4
Method BLASTX
NCBI GI g132105
BLAST score 794
E value 5.0e-85
Match length 168
% identity 90
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

this gene. [Arabidopsis thaliana]

Seq. No. 401638
Seq. ID LIB3431-045-P1-K1-F12
Method BLASTN
NCBI GI g2073379
BLAST score 165
E value 9.0e-88
Match length 203
% identity 95
NCBI Description Rice CP26 mRNA, partial sequence

Seq. No. 401639
Seq. ID LIB3431-045-P1-K1-F3
Method BLASTX
NCBI GI g3126854
BLAST score 751
E value 8.0e-82
Match length 156
% identity 97
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401640
Seq. ID LIB3431-045-P1-K1-F4
Method BLASTX
NCBI GI g3126854
BLAST score 613
E value 7.0e-64
Match length 117
% identity 99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401641
Seq. ID LIB3431-045-P1-K1-F6
Method BLASTN
NCBI GI g3618309
BLAST score 45
E value 3.0e-16
Match length 65
% identity 94
NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds, clone:E10707

Seq. No. 401642
Seq. ID LIB3431-045-P1-K1-F8
Method BLASTX
NCBI GI g4587556
BLAST score 168
E value 8.0e-12
Match length 44
% identity 75
NCBI Description (AC006577) Similar to gi_1653162 (p)ppGpp 3-pyrophosphohydrolase from Synechocystis sp genome gb_D90911. EST gb_W43807 comes from this gene. [Arabidopsis thaliana]

Seq. No. 401643

complete cds

Seq. No. 401679
Seq. ID LIB3431-045-P1-N1-D3
Method BLASTN
NCBI GI g3789953
BLAST score 228
E value 1.0e-125
Match length 268
% identity 96
NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 401680
Seq. ID LIB3431-045-P1-N1-D5
Method BLASTX
NCBI GI g671740
BLAST score 326
E value 3.0e-30
Match length 61
% identity 100
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401681
Seq. ID LIB3431-045-P1-N1-D6
Method BLASTN
NCBI GI g2072554
BLAST score 392
E value 0.0e+00
Match length 407
% identity 99
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401682
Seq. ID LIB3431-045-P1-N1-D8
Method BLASTX
NCBI GI g115787
BLAST score 403
E value 3.0e-39
Match length 76
% identity 100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401683
Seq. ID LIB3431-045-P1-N1-E11
Method BLASTX
NCBI GI g2274988
BLAST score 291
E value 4.0e-26
Match length 74


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Seq. ID      LIB3431-046-P1-K1-A7
Method       BLASTX
NCBI GI      g3075488
BLAST score   545
E value      5.0e-56
Match length 107
% identity    98
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
```

```
Seq. No.          401715
Seq. ID           LIB3431-046-P1-K1-A8
Method            BLASTX
NCBI GI           g100454
BLAST score       627
E value           2.0e-65
Match length      154
% identity        77
NCBI Description   photosystem II oxygen-evolving complex protein 1 - potato
                   >gi_809113_emb_CAA35601_ (X17578): 33kDa precursor protein
                   of oxygen-evolving complex [Solanum tuberosum]
```

Seq. No.	401716
Seq. ID	LIB3431-046-P1-K1-B10
Method	BLASTX
NCBI GI	g6093830
BLAST score	155
E value	2.0e-10
Match length	37
% identity	81
NCBI Description	PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]

```
Seq. No.      401717
Seq. ID      LIB3431-046-P1-K1-B11
Method       BLASTX
NCBI GI      g82080
BLAST score   433
E value      9.0e-43
Match length  124
% identity    67
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
                >gi_226872_prf_1609235A chlorophyll a/b binding protein
                [Lycopersicon esculentum]
```

Seq. No.	401718
Seq. ID	LIB3431-046-P1-K1-B12
Method	BLASTX
NCBI GI	g3395439
BLAST score	266
E value	4.0e-23
Match length	81
% identity	62
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 401719

Seq. ID LIB3431-046-P1-K1-D6
 Method BLASTX
 NCBI GI g2072555
 BLAST score 175
 E value 1.0e-12
 Match length 32
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 401735
 Seq. ID LIB3431-046-P1-K1-D8
 Method BLASTX
 NCBI GI g1519249
 BLAST score 697
 E value 1.0e-73
 Match length 146
 % identity 95
 NCBI Description (U65956) GF14-b protein [Oryza sativa]

Seq. No. 401736
 Seq. ID LIB3431-046-P1-K1-D9
 Method BLASTX
 NCBI GI g5738522
 BLAST score 180
 E value 2.0e-13
 Match length 50
 % identity 72
 NCBI Description (AL109846) putative pre-mrna splicing factor atp-dependent
 rna helicase [Schizosaccharomyces pombe]

Seq. No. 401737
 Seq. ID LIB3431-046-P1-K1-E1
 Method BLASTX
 NCBI GI g417260
 BLAST score 381
 E value 1.0e-36
 Match length 121
 % identity 64
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 401738
 Seq. ID LIB3431-046-P1-K1-E12
 Method BLASTX
 NCBI GI g115787
 BLAST score 540
 E value 2.0e-55
 Match length 123
 % identity 88
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109_
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Match length 103
 % identity 76
 NCBI Description SUPEROXIDE DISMUTASE-2 [CU-ZN] >gi_2660798 (AF034832)
 cytosolic copper/zinc superoxide dismutase
 [Mesembryanthemum crystallinum]

Seq. No. 401744
 Seq. ID LIB3431-046-P1-K1-E8
 Method BLASTX
 NCBI GI g3789954
 BLAST score 563
 E value 4.0e-58
 Match length 120
 % identity 88
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 401745
 Seq. ID LIB3431-046-P1-K1-E9
 Method BLASTX
 NCBI GI g4587556
 BLAST score 284
 E value 2.0e-25
 Match length 103
 % identity 53
 NCBI Description (AC006577) Similar to gi_1653162 (p)ppGpp
 3-pyrophosphohydrolase from Synechocystis sp genome
 gb_D90911. EST gb_W43807 comes from this gene.
 [Arabidopsis thaliana]

Seq. No. 401746
 Seq. ID LIB3431-046-P1-K1-F1
 Method BLASTX
 NCBI GI g115787
 BLAST score 529
 E value 5.0e-54
 Match length 121
 % identity 88
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 401747
 Seq. ID LIB3431-046-P1-K1-F11
 Method BLASTX
 NCBI GI g3345477
 BLAST score 707
 E value 7.0e-75
 Match length 151
 % identity 90
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 401748
 Seq. ID LIB3431-046-P1-K1-F3
 Method BLASTX

Seq. ID	LIB3431-046-P1-K1-H10
Method	BLASTX
NCBI GI	g3345477
BLAST score	564
E value	5.0e-58
Match length	106
% identity	100
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

```
Seq. No.      401763
Seq. ID      LIB3431-046-P1-K1-H2
Method       BLASTX
NCBI GI      g2072555
BLAST score   237
E value      9.0e-20
Match length  44
% identity    100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
               >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
               protein [Oryza sativa]
```

```
Seq. No.      401764
Seq. ID      LIB3431-046-P1-K1-H3
Method       BLASTX
NCBI GI      g399213
BLAST score   781
E value      2.0e-83
Match length  170
% identity    91
NCBI Description  ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
CD4B PRECURSOR >gi_100190_pir_B35905 CD4B protein - tomato
>gi_170435 (M32604) ATP-dependent protease (CD4B)
[Lycopersicon esculentum]
```

```
Seq. No.      401765
Seq. ID       LIB3431-046-P1-K1-H4
Method        BLASTX
NCBI GI       g4079798
BLAST score    408
E value        8.0e-40
Match length   112
% identity     72
NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza
sativa]
```

```
Seq. No.          401766
Seq. ID           LIB3431-046-P1-K1-H6
Method            BLASTX
NCBI GI           g118170
BLAST score       429
E value           4.0e-42
Match length      102
% identity        85
NCBI Description   CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I)
                  >gi_82491_pir_A28464 oryzacystatin - rice >gi_169784
                  (J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259)
                  oryzastatin [Oryza sativa] >gi_259137 bbs_120195 (S49967)
```


Seq. ID	LIB3431-046-P1-N1-A11
Method	BLASTN
NCBI GI	g4105560
BLAST score	101
E value	2.0e-49
Match length	164
% identity	90
NCBI Description	Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA, complete cds
Seq. No.	401772
Seq. ID	LIB3431-046-P1-N1-A4
Method	BLASTX
NCBI GI	g2288969
BLAST score	205
E value	5.0e-16
Match length	68
% identity	54
NCBI Description	(Y12862) glutathione transferase [Zea mays]
Seq. No.	401773
Seq. ID	LIB3431-046-P1-N1-A6
Method	BLASTX
NCBI GI	g115787
BLAST score	409
E value	6.0e-40
Match length	77
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]
Seq. No.	401774
Seq. ID	LIB3431-046-P1-N1-A7
Method	BLASTX
NCBI GI	g2326947
BLAST score	224
E value	3.0e-18
Match length	44
% identity	98
NCBI Description	(Z50801) Chlorophyll a/b-binding protein CP29 precursor [Zea mays]
Seq. No.	401775
Seq. ID	LIB3431-046-P1-N1-A8
Method	BLASTX
NCBI GI	g482311
BLAST score	244
E value	9.0e-21
Match length	50
% identity	96
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]

CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
chlorophyll a/b-binding protein [*Lycopersicon esculentum*]

Seq. No.	401802
Seq. ID	LIB3431-046-P1-N1-F5
Method	BLASTX
NCBI GI	g1835731
BLAST score	371
E value	2.0e-35
Match length	82
% identity	88
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

```
Seq. No.      401803
Seq. ID      LIB3431-046-P1-N1-F6
Method       BLASTX
NCBI GI      g421916
BLAST score   178
E value      6.0e-13
Match length  32
% identity    100
NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)
                >gi_12582 emb_CAA48410_ (X68333) light harvesting
                chlorophyll a/b binding protein [Hedera helix]
```

```
Seq. No.      401804
Seq. ID      LIB3431-046-P1-N1-F8
Method       BLASTX
NCBI GI      g100614
BLAST score   196
E value      3.0e-15
Match length  50
% identity    78
NCBI Description  ribulose-bisphosphate carboxylase activase A long form
                  precursor - barley (fragment) >gi_167089 (M55446) ribulose
                  1,5-bisphosphate carboxylase activase [Hordeum vulgare]
```

```
Seq. No.      401805
Seq. ID      LIB3431-046-P1-N1-G10
Method       BLASTX
NCBI GI      g347451
BLAST score   236
E value      9.0e-20
Match length  47
% identity    98
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
sativa]
```

Seq. No.	401806
Seq. ID	LIB3431-046-P1-N1-G11
Method	BLASTX
NCBI GI	g3914470
BLAST score	374
E value	4.0e-39
Match length	105
% identity	68
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

NCBI Description Sorghum bicolor BAC clone 25.M18, complete sequence

Seq. No.	401812
Seq. ID	LIB3431-046-P1-N1-H10
Method	BLASTN
NCBI GI	g606816
BLAST score	184
E value	3.0e-99
Match length	208
% identity	97
NCBI Description	Oryza sativa chloroplast carbonic anhydrase mRNA, complete cds

Seq. No.	401813
Seq. ID	LIB3431-046-P1-N1-H4
Method	BLASTN
NCBI GI	g1398998
BLAST score	165
E value	9.0e-88
Match length	272
% identity	97
NCBI Description	Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II, complete cds

```
Seq. No.          401814
Seq. ID          LIB3431-046-P1-N1-H7
Method           BLASTX
NCBI GI          g1173347
BLAST score      172
E value          3.0e-12
Match length     39
% identity       92
NCBI Description  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                  (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
```

Seq. No.	401815
Seq. ID	LIB3431-046-P1-N1-H9
Method	BLASTN
NCBI GI	g2661765
BLAST score	46
E value	1.0e-16
Match length	82
% identity	89
NCBI Description	Zea mays mRNA for putative porphobilinogen deaminase

Seq. No.	401816
Seq. ID	LIB3431-047-P1-K1-A11
Method	BLASTX
NCBI GI	g482311
BLAST score	649
E value	4.0e-68
Match length	129
% identity	98

NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
 (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving
 complex protein 1 [Oryza sativa]

```
Seq. No.          401817
Seq. ID           LIB3431-047-P1-K1-A12
Method            BLASTN
NCBI GI           g20262
BLAST score       252
E value           1.0e-139
Match length      252
% identity        100
NCBI Description   O.sativa light-induced mRNA
```

```
Seq. No.      401818
Seq. ID      LIB3431-047-P1-K1-A3
Method       BLASTX
NCBI GI      g5912299
BLAST score   547
E value      3.0e-56
Match length  105
% identity    100
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
```

```
Seq. No.      201819
Seq. ID       LIB3431-047-P1-K1-A4
Method        BLASTX
NCBI GI       g132105
BLAST score    533
E value        2.0e-54
Match length   118
% identity     86
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                carboxylase S [Oryza sativa]
```

Seq. No.	401820
Seq. ID	LIB3431-047-P1-K1-A5
Method	BLASTX
NCBI GI	g22240
BLAST score	450
E value	7.0e-45
Match length	116
% identity	79
NCBI Description	(X07157) GADPH (383 AA) [Zea mays]

```
Seq. No.      401821
Seq. ID      LIB3431-047-P1-K1-A7
Method       BLASTX
NCBI GI      g6016875
BLAST score  275
```


E value	0.0e+00
Match length	369
% identity	98
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

```

Seq. No.          401846
Seq. ID           LIB3431-047-P1-K1-D3
Method            BLASTX
NCBI GI           g132105
BLAST score       532
E value           2.0e-54
Match length      122
% identity        83
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

```

```
Seq. No.      401847
Seq. ID      LIB3431-047-P1-K1-D4
Method       BLASTX
NCBI GI      g534982
BLAST score   264
E value      5.0e-37
Match length  126
% identity    56
NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]
```

```
Seq. No.      401848
Seq. ID      LIB3431-047-P1-K1-D7
Method       BLASTX
NCBI GI      g729478
BLAST score   476
E value      7.0e-48
Match length 102
% identity    85
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
>gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
(AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to
a region of the predicted gene.; similar to
ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
```

```
Seq. No.      401849
Seq. ID      LIB3431-047-P1-K1-E1
Method       BLASTX
NCBI GI      g115787
BLAST score   349
E value       4.0e-33
Match length  86
% identity    84
```


NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

```
Seq. No.          401850
Seq. ID           LIB3431-047-P1-K1-E10
Method            BLASTX
NCBI GI           g3913018
BLAST score       876
E value           1.0e-94
Match length      171
% identity        98
```

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
(ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
aldolase [*Oryza sativa*]

Seq. No.	401851
Seq. ID	LIB3431-047-P1-K1-E11
Method	BLASTX
NCBI GI	g6063542
BLAST score	768
E value	5.0e-82
Match length	151
% identity	99
NCBI Description	(AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

```
Seq. No.          401852
Seq. ID           LIB3431-047-P1-K1-E12
Method            BLASTX
NCBI GI           g1617197
BLAST score       304
E value           1.0e-27
Match length      76
% identity        76
NCBI Description   (Z72488) CP12 [Nicotiana tabacum]
```

```
Seq. No.          401853
Seq. ID           LIB3431-047-P1-K1-E2
Method            BLASTN
NCBI GI           g6103440
BLAST score       268
E value           1.0e-149
Match length      278
% identity         99
NCBI Description   Oryza sativa metallothionein-like protein (ML2) mRNA,
                  complete cds
```

```
Seq. No.      401854
Seq. ID      LIB3431-047-P1-K1-E3
Method       BLASTN
NCBI GI      g6015437
BLAST score   36
E value      6.0e-11
```



```
Seq. No.      401860
Seq. ID      LIB3431-047-P1-K1-F2
Method       BLASTX
NCBI GI      g3915131
BLAST score   242
E value      9.0e-21
Match length  48
% identity    100
NCBI Description  THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
                >gi_426442_dbj_BAA04864_(D21836) thioredoxin h [Oryza
                sativa] >gi_454882_dbj_BAA05546_(D26547) rice thioredoxin
                h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza
                sativa]
```

```
Seq. No.          401861
Seq. ID           LIB3431-047-P1-K1-F4
Method            BLASTN
NCBI GI           g1103627
BLAST score       57
E value           3.0e-23
Match length      85
% identity        92
NCBI Description   Z.mays Fer1 gene
```

```
Seq. No.      401862
Seq. ID       LIB3431-047-P1-K1-F5
Method        BLASTX
NCBI GI       g3309269
BLAST score    448
E value       2.0e-44
Match length   107
% identity     80
NCBI Description (AF074940) ferric leghemoglobin reductase-2 precursor
               [Glycine max]
```

```
Seq. No.          401863
Seq. ID           LIB3431-047-P1-K1-F6
Method            BLASTX
NCBI GI           g4587615
BLAST score       453
E value           1.0e-49
Match length      135
% identity        71
NCBI Description  (AC006951) putative acyl-CoA synthetase [Arabidopsis
                  thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213)
                  putative acyl-CoA synthetase [Arabidopsis thaliana]
```

```
Seq. No.      401864
Seq. ID      LIB3431-047-P1-K1-F8
Method       BLASTX
NCBI GI      g3789954
BLAST score   199
E value      6.0e-16
Match length  46
% identity    83
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
sativa]
```



```
Seq. No.      401865
Seq. ID      LIB3431-047-P1-K1-F9
Method       BLASTX
NCBI GI      g115787
BLAST score   504
E value      4.0e-51
Match length  118
% identity    86
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109_
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

```
Seq. No.      401866
Seq. ID      LIB3431-047-P1-K1-G11
Method       BLASTX
NCBI GI      g132105
BLAST score   470
E value      3.0e-47
Match length  107
% identity    85
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                carboxylase S [Oryza sativa]
```

```
Seq. No.      401867
Seq. ID      LIB3431-047-P1-K1-G12
Method       BLASTX
NCBI GI      g3345477
BLAST score   315
E value      5.0e-29
Match length  109
% identity    59
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
```

```

Seq. No.      401868
Seq. ID       LIB3431-047-P1-K1-G2
Method        BLASTX
NCBI GI       g115771
BLAST score   864
E value       3.0e-93
Match length  170
% identity    95
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
                  CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding
                  protein precursor - maize >gi_22224_emb_CAA32900_ (X14794)
                  chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

```

Seq. No. 401869

% identity	98
NCBI Description	Oryza sativa Ca2+-ATPase gene, complete cds
Seq. No.	401895
Seq. ID	LIB3431-047-P1-N1-B5
Method	BLASTX
NCBI GI	g671740
BLAST score	243
E value	2.0e-20
Match length	47
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]
Seq. No.	401896
Seq. ID	LIB3431-047-P1-N1-B7
Method	BLASTN
NCBI GI	g218209
BLAST score	59
E value	2.0e-24
Match length	75
% identity	95
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106
Seq. No.	401897
Seq. ID	LIB3431-047-P1-N1-B9
Method	BLASTN
NCBI GI	g3885887
BLAST score	298
E value	1.0e-167
Match length	349
% identity	96
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds
Seq. No.	401898
Seq. ID	LIB3431-047-P1-N1-C10
Method	BLASTN
NCBI GI	g5714761
BLAST score	54
E value	2.0e-21
Match length	78
% identity	92
NCBI Description	Oryza sativa subsp. indica serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete cds
Seq. No.	401899
Seq. ID	LIB3431-047-P1-N1-C11
Method	BLASTN
NCBI GI	g3819352
BLAST score	58
E value	8.0e-24
Match length	82
% identity	93


```
Seq. No.          401905
Seq. ID           LIB3431-047-P1-N1-C7
Method            BLASTX
NCBI GI           g2072555
BLAST score       230
E value           6.0e-19
Match length      44
% identity        98
NCBI Description   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
```

Seq. No.	401906
Seq. ID	LIB3431-047-P1-N1-C8
Method	BLASTX
NCBI GI	g167097
BLAST score	189
E value	6.0e-26
Match length	74
% identity	82
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	401907
Seq. ID	LIB3431-047-P1-N1-D11
Method	BLASTN
NCBI GI	g2570514
BLAST score	312
E value	1.0e-175
Match length	370
% identity	96
NCBI Description	Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No.	401908
Seq. ID	LIB3431-047-P1-N1-D2
Method	BLASTN
NCBI GI	g20181
BLAST score	142
E value	5.0e-74
Match length	156
% identity	97
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

```
Seq. No.      401909
Seq. ID      LIB3431-047-P1-N1-D3
Method       BLASTX
NCBI GI      g132105
BLAST score   360
E value      4.0e-34
Match length  67
% identity    99
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538
```


(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose biphosphate carboxylase S [Oryza sativa]

```
Seq. No.      401910
Seq. ID       LIB3431-047-P1-N1-D4
Method        BLASTX
NCBI GI       g534982
BLAST score    214
E value        2.0e-32
Match length   106
% identity     58
NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]
```

```
Seq. No.          401911
Seq. ID           LIB3431-047-P1-N1-D6
Method            BLASTX
NCBI GI           g114622
BLAST score       249
E value           4.0e-21
Match length      53
% identity        92
NCBI Description  ATP SYNTHASE B CHAIN (SUBUNIT I) >gi_67929_pir_LWRZ1
                  H+-transporting ATP synthase (EC 3.6.1.34) chain I - rice
                  chloroplast >gi_669080_emb_CAA33992_ (X15901) ATPase I
                  subunit [Oryza sativa] >gi_226695_prf_1603356W ATPase I
                  [Oryza sativa]
```

```
Seq. No.      401912
Seq. ID      LIB3431-047-P1-N1-D7
Method       BLASTX
NCBI GI      g729478
BLAST score   398
E value      1.0e-38
Match length  81
% identity    90
NCBI Description  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
                >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
                reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
                (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to
                a region of the predicted gene.; similar to
                ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
```

```
Seq. No.          401913
Seq. ID           LIB3431-047-P1-N1-D8
Method            BLASTX
NCBI GI           g5911312
BLAST score       466
E value           1.0e-46
Match length      105
% identity        80
NCBI Description  (AF026167) ankyrin repeat protein EMB506 [Arabidopsis
                  thaliana]
```

Seq. No. 401914

NCBI GI	g3345476
BLAST score	244
E value	1.0e-135
Match length	307
% identity	95
NCBI Description	Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No.	401930
Seq. ID	LIB3431-047-P1-N1-G2
Method	BLASTN
NCBI GI	g20181
BLAST score	56
E value	7.0e-23
Match length	67
% identity	96
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

```
Seq. No.          401931
Seq. ID           LIB3431-047-P1-N1-G4
Method            BLASTX
NCBI GI           g4204276
BLAST score       226
E value           2.0e-18
Match length      73
% identity        58
NCBI Description   (AC004146) Hypothetical protein [Arabidopsis thaliana]
```

Seq. No.	401932
Seq. ID	LIB3431-047-P1-N1-G5
Method	BLASTX
NCBI GI	g4689380
BLAST score	260
E value	9.0e-23
Match length	55
% identity	91
NCBI Description	(AF139465) LHCII type III chlorophyll a/b binding protein [Vigna radiata]

```
Seq. No.          401933
Seq. ID          LIB3431-047-P1-N1-G7
Method          BLASTX
NCBI GI         g115802
BLAST score      187
E value         3.0e-14
Match length     36
% identity       97
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
                CAB-36) (LHCP) >gi_100311_pir_S21827 chlorophyll
                a/b-binding protein (cab-36) - common tobacco
                >gi_19827_emb_CAA41188_(X58230) chlorophyll a/b binding
                protein [Nicotiana tabacum]
```

```
Seq. No.      401934
Seq. ID      LIB3431-047-P1-N1-G9
Method       BLASTX
NCBI GI      q122106
```


[illegible]

```
Seq. No.      401944
Seq. ID      LIB3431-048-P1-K1-B5
Method       BLASTN
NCBI GI      g20369
BLAST score   143
E value      7.0e-75
Match length  158
% identity    97
NCBI Description  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
synthetase (EC 6.3.1.2) (clone lambda-GS31)
>gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of
chloroplast localising glutamine synthetase
```

```
Seq. No.          401946
Seq. ID          LIB3431-048-P1-K1-B8
Method           BLASTX
NCBI GI         g115772
BLAST score      174
E value         5.0e-13
Match length     40
% identity       93
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
                CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding
                protein 1R precursor - rice >gi_20178_emb_CAA32108_
                (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                [Oryza sativa]
```

51590


```
BLAST score      258
E value         7.0e-23
Match length    54
% identity      94
NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                 (AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein -
                 rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                 sativa]
```

```
Seq. No.      401959
Seq. ID      LIB3431-048-P1-K1-E1
Method       BLASTX
NCBI GI      g5630087
BLAST score   200
E value      1.0e-15
Match length  111
% identity    41
NCBI Description (AC004876) similar to predicted proteins AAB54240
(PID:g2088822) and S67138 (PID:g2132925) [Homo sapiens]
```

Seq. No.	401960
Seq. ID	LIB3431-048-P1-K1-E11
Method	BLASTN
NCBI GI	g304219
BLAST score	80
E value	4.0e-37
Match length	199
% identity	85
NCBI Description	Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No.	401961
Seq. ID	LIB3431-048-P1-K1-E2
Method	BLASTN
NCBI GI	g4959460
BLAST score	38
E value	3.0e-12
Match length	38
% identity	100
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

```
Seq. No.          401962
Seq. ID           LIB3431-048-P1-K1-E4
Method            BLASTX
NCBI GI           g132105
BLAST score       222
E value           1.0e-18
Match length      63
% identity        73
NCBI Description  RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375 prf_1508256A ribulose bisphosphate
```


[illegible]

Seq. No. 401968
Seq. ID LIB3431-048-P1-K1-F7

Method	BLASTX
NCBI GI	g3126854
BLAST score	151
E value	4.0e-10
Match length	33
% identity	91
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	401969
Seq. ID	LIB3431-048-P1-K1-G10
Method	BLASTX
NCBI GI	g733454
BLAST score	266
E value	2.0e-23
Match length	74
% identity	73
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]
Seq. No.	401970
Seq. ID	LIB3431-048-P1-K1-G12
Method	BLASTX
NCBI GI	g2501189
BLAST score	444
E value	2.0e-44
Match length	90
% identity	94
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme [Zea mays]
Seq. No.	401971
Seq. ID	LIB3431-048-P1-K1-G4
Method	BLASTX
NCBI GI	g671740
BLAST score	416
E value	6.0e-41
Match length	75
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]
Seq. No.	401972
Seq. ID	LIB3431-048-P1-K1-G9
Method	BLASTN
NCBI GI	g218207
BLAST score	104
E value	9.0e-52
Match length	112
% identity	98
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139
Seq. No.	401973
Seq. ID	LIB3431-048-P1-K1-H1

Match length	60
% identity	95
NCBI Description	plastocyanin precursor - barley >gi_22705_emb_CAA68696_ (Y00704) plastocyanin precursor [Hordeum vulgare] >gi_431920_emb_CAA82201_ (Z28347) plastocyanin [Hordeum vulgare]
Seq. No.	401988
Seq. ID	LIB3431-048-P1-N1-B5
Method	BLASTN
NCBI GI	g20369
BLAST score	321
E value	0.0e+00
Match length	355
% identity	98
NCBI Description	Oryza sativa shoot GS2 mRNA for chloroplastic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS31) >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of chloroplast localising glutamine synthetase
Seq. No.	401989
Seq. ID	LIB3431-048-P1-N1-B7
Method	BLASTX
NCBI GI	g3789954
BLAST score	299
E value	5.0e-27
Match length	57
% identity	98
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]
Seq. No.	401990
Seq. ID	LIB3431-048-P1-N1-B8
Method	BLASTX
NCBI GI	g3036946
BLAST score	301
E value	2.0e-27
Match length	61
% identity	95
NCBI Description	(AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana glauca]
Seq. No.	401991
Seq. ID	LIB3431-048-P1-N1-B9
Method	BLASTX
NCBI GI	g2696804
BLAST score	406
E value	1.0e-39
Match length	79
% identity	95
NCBI Description	(AB009665) water channel protein [Oryza sativa]
Seq. No.	401992
Seq. ID	LIB3431-048-P1-N1-C12
Method	BLASTX
NCBI GI	g1917019
BLAST score	195

a region of the predicted gene.; similar to
ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 402022
Seq. ID LIB3431-048-P1-N1-H12
Method BLASTX
NCBI GI g1170937
BLAST score 189
E value 3.0e-14
Match length 33
% identity 100
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
synthetase [Oryza sativa]

Seq. No. 402023
Seq. ID LIB3431-048-P1-N1-H2
Method BLASTX
NCBI GI g3345477
BLAST score 346
E value 2.0e-32
Match length 66
% identity 98
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 402024
Seq. ID LIB3431-048-P1-N1-H3
Method BLASTX
NCBI GI g1235664
BLAST score 314
E value 7.0e-29
Match length 88
% identity 75
NCBI Description (U37936) novel calmodulin-like protein [Oryza sativa]
>gi_3171148 (AF064456) calmodulin-like protein [Oryza
sativa subsp. indica]

Seq. No. 402025
Seq. ID LIB3431-048-P1-N1-H5
Method BLASTX
NCBI GI g3063710
BLAST score 175
E value 2.0e-12
Match length 35
% identity 80
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 402026
Seq. ID LIB3431-049-P1-K1-A10
Method BLASTN
NCBI GI g20181
BLAST score 71
E value 4.0e-32
Match length 113
% identity 93
NCBI Description Rice cab2R gene for light harvesting chlorophyll

a/b-binding protein

```
Seq. No.      402027
Seq. ID      LIB3431-049-P1-K1-A2
Method       BLASTX
NCBI GI      g4510363
BLAST score   242
E value      5.0e-21
Match length  50
% identity    86
NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis
thaliana]
```

```
Seq. No.      402029
Seq. ID      LIB3431-049-P1-K1-B12
Method       BLASTX
NCBI GI      g606817
BLAST score   295
E value      2.0e-32
Match length  87
% identity    86
NCBI Description (U08404) carbonic anhydrase [Oryza sativa]
               >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic
               anhydrase 3 [Oryza sativa]
```

Seq. No.	402031
Seq. ID	LIB3431-049-P1-K1-B3
Method	BLASTN
NCBI GI	g20181
BLAST score	48
E value	2.0e-18
Match length	72
% identity	92
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. ID	LIB3431-049-P1-K1-D4
Method	BLASTX
NCBI GI	g3126854
BLAST score	345
E value	6.0e-35
Match length	78
% identity	97
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

```
Seq. No.          402043
Seq. ID           LIB3431-049-P1-K1-E10
Method            BLASTN
NCBI GI           g3126853
BLAST score       150
E value           6.0e-79
Match length      222
% identity        93
NCBI Description  Oryza sativa chlorophyll a/b binding protein (RCABP89)
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  cds
```

Seq. No.	402044
Seq. ID	LIB3431-049-P1-K1-E11
Method	BLASTN
NCBI GI	g4138289
BLAST score	68
E value	4.0e-30
Match length	72
% identity	99
NCBI Description	Oryza sativa mRNA for thioredoxin M

Seq. No.	402045
Seq. ID	LIB3431-049-P1-K1-E9
Method	BLASTN
NCBI GI	g3885891
BLAST score	80
E value	7.0e-37
Match length	95
% identity	97
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	402046
Seq. ID	LIB3431-049-P1-K1-F12
Method	BLASTX
NCBI GI	g3885894
BLAST score	266
E value	9.0e-34
Match length	91
% identity	86
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

```
Seq. No.      402047
Seq. ID      LIB3431-049-P1-K1-F2
Method       BLASTX
NCBI GI      g2130089
BLAST score  219
```

Parameter	Value	Unit
Temperature	25	°C
Pressure	1	atm
Time	10	min
Concentration	0.1	M
Volume	10	L
Mass	10	g
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	J
Power	10	W
Frequency	10	Hz
Wavelength	10	nm
Angle	10	°
Distance	10	m
Speed	10	m/s
Acceleration	10	m/s ²
Force	10	N
Momentum	10	kg·m/s
Energy	10	


```
Seq. No.      402083
Seq. ID      LIB3431-049-P1-N1-F4
Method       BLASTX
NCBI GI      g320618
BLAST score   241
E value      2.0e-20
Match length  54
% identity    87
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
```

```
Seq. No.      402084
Seq. ID      LIB3431-049-P1-N1-F6
Method       BLASTN
NCBI GI      g409581
BLAST score   416
E value      0.0e+00
Match length  452
% identity    98
NCBI Description  Rice mRNA for serine carboxypeptidase-like protein
```

```
Seq. No.      402085
Seq. ID      LIB3431-049-P1-N1-F8
Method       BLASTX
NCBI GI      g671740
BLAST score   252
E value      1.0e-21
Match length  57
% identity    82
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]
```

Seq. No.	402086
Seq. ID	LIB3431-049-P1-N1-F9
Method	BLASTX
NCBI GI	g829283
BLAST score	273
E value	5.0e-24
Match length	68
% identity	82
NCBI Description	(Z15018) heat shock protein hsp82 [Oryza sativa]

Seq. No.	402087
Seq. ID	LIB3431-049-P1-N1-G2
Method	BLASTX
NCBI GI	g3885892
BLAST score	389
E value	1.0e-37
Match length	75
% identity	100
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402088

[illegible]

sativa] >gi_226375_prf_1508256A ribulose biphosphate
carboxylase S [Oryza sativa]

Seq. No. 402098
Seq. ID LIB3431-050-P1-K1-A5
Method BLASTX
NCBI GI g671740
BLAST score 449
E value 1.0e-44
Match length 83
% identity 99
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]

Seq. No. 402099
Seq. ID LIB3431-050-P1-K1-A6
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 6.0e-20
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]

Seq. No. 402100
Seq. ID LIB3431-050-P1-K1-A7
Method BLASTX
NCBI GI g1170507
BLAST score 627
E value 2.0e-65
Match length 130
% identity 92
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)
>gi_100276_pir_S22579 translation initiation factor eIF-4A
- curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206)
nicotiana eukaryotic translation initiation factor 4A
[Nicotiana plumbaginifolia]

Seq. No. 402101
Seq. ID LIB3431-050-P1-K1-A8
Method BLASTX
NCBI GI g3080391
BLAST score 526
E value 1.0e-53
Match length 125
% identity 76
NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 402102
Seq. ID LIB3431-050-P1-K1-B1
Method BLASTN
NCBI GI g218207
BLAST score 101
E value 2.0e-49
Match length 116

this gene

Seq. No. 402152
Seq. ID LIB3431-050-P1-N1-B2
Method BLASTX
NCBI GI g115787
BLAST score 480
E value 3.0e-48
Match length 92
% identity 99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 402153
Seq. ID LIB3431-050-P1-N1-B5
Method BLASTX
NCBI GI g1429226
BLAST score 228
E value 1.0e-18
Match length 47
% identity 85
NCBI Description (X98861) TFIIA [Arabidopsis thaliana]

Seq. No. 402154
Seq. ID LIB3431-050-P1-N1-B8
Method BLASTX
NCBI GI g5729802
BLAST score 452
E value 6.0e-45
Match length 91
% identity 89
NCBI Description similar to S. pombe dim1+ >gi_2565275 (AF023611) Dim1p homolog [Homo sapiens]

Seq. No. 402155
Seq. ID LIB3431-050-P1-N1-C1
Method BLASTX
NCBI GI g3236242
BLAST score 334
E value 4.0e-31
Match length 98
% identity 69
NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No. 402156
Seq. ID LIB3431-050-P1-N1-C11
Method BLASTX
NCBI GI g131176
BLAST score 203
E value 6.0e-16
Match length 47
% identity 87
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR

(PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
>gi_72683_pir_F1BH4 photosystem I chain IV precursor -
barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
-46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A
10.8kD photosystem I protein [Hordeum vulgare var.
distichum]

Seq. No. 402157
Seq. ID LIB3431-050-P1-N1-C12
Method BLASTX
NCBI GI g115813
BLAST score 201
E value 1.0e-15
Match length 46
% identity 80
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402158
Seq. ID LIB3431-050-P1-N1-C2
Method BLASTX
NCBI GI g289920
BLAST score 267
E value 3.0e-23
Match length 51
% identity 98
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
hirsutum]

Seq. No. 402159
Seq. ID LIB3431-050-P1-N1-C4
Method BLASTX
NCBI GI g2492487
BLAST score 330
E value 1.0e-30
Match length 76
% identity 87
NCBI Description 14-3-3-LIKE PROTEIN B (14-3-3B) >gi_1070354_emb_CAA63658_
(X93170) Hv14-3-3b [Hordeum vulgare]

Seq. No. 402160
Seq. ID LIB3431-050-P1-N1-C9
Method BLASTN
NCBI GI g218207
BLAST score 124
E value 2.0e-63
Match length 231
% identity 88
NCBI Description Oryza sativa mRNA for the small subunit of
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
pOSSS1139

Seq. No. 402161
Seq. ID LIB3431-050-P1-N1-D1
Method BLASTN
NCBI GI g3868755

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 91R PRECURSOR (LHCII TYPE I CAB-91R) (LHCP) >gi_72732_pir_CDPJ91 chlorophyll a/b-binding protein 91R precursor - petunia
>gi_20487_emb_CAA26209_ (X02356) cab 91R precursor polypeptide (aa -34 to 233) [Petunia sp.]

Seq. No. 402222
Seq. ID LIB3431-051-P1-K1-F10
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 1.0e-19
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402223
Seq. ID LIB3431-051-P1-K1-F11
Method BLASTX
NCBI GI g320618
BLAST score 542
E value 2.0e-56
Match length 133
% identity 86
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 402224
Seq. ID LIB3431-051-P1-K1-F3
Method BLASTN
NCBI GI g3789951
BLAST score 254
E value 1.0e-141
Match length 297
% identity 97
NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 402225
Seq. ID LIB3431-051-P1-K1-F4
Method BLASTX
NCBI GI g3913018
BLAST score 565
E value 2.0e-58
Match length 116
% identity 94
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No. 402226

[illegible]

```
Seq. No.      402267
Seq. ID      LIB3431-051-P1-N1-D12
Method       BLASTX
NCBI GI      g5106775
BLAST score   259
E value      2.0e-22
Match length  52
% identity    92
NCBI Description (AF067732) ribosomal protein S12 [Hordeum vulgare]
```

Seq. No.	402269
Seq. ID	LIB3431-051-P1-N1-D5
Method	BLASTX
NCBI GI	g167097
BLAST score	142
E value	7.0e-09
Match length	30
% identity	83
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	402270
Seq. ID	LIB3431-051-P1-N1-D6
Method	BLASTN
NCBI GI	g3377792
BLAST score	97
E value	4.0e-47
Match length	267
% identity	84
NCBI Description	Oryza sativa ribulose-1,5-bisphosphate

Seq. No.	402271
Seq. ID	LIB3431-051-P1-N1-D8
Method	BLASTN
NCBI GI	g416266
BLAST score	211
E value	1.0e-115
Match length	269
% identity	94
NCBI Description	Rice mRNA for oxygen-evolving protein, partial sequence

```
Seq. No.      402272
Seq. ID      LIB3431-051-P1-N1-D9
Method       BLASTX
NCBI GI      g733454
BLAST score   158
E value      8.0e-11
Match length  45
% identity    69
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
               [Zea mays]
```

```
Seq. No.      402273
Seq. ID      LIB3431-051-P1-N1-E1
Method       BLASTX
NCBI GI      g2961176
BLAST score   322
E value      7.0e-30
Match length  81
% identity    80
NCBI Description (AF050674) ribosomal protein L27 precursor [Oryza sativa]
```

```
Seq. No.      402274
Seq. ID      LIB3431-051-P1-N1-E10
Method       BLASTX
NCBI GI      g3928140
BLAST score   166
E value      1.0e-11
Match length  34
% identity    88
NCBI Description (AJ131044) chlorophyll a/b binding protein [Cicer
arietinum]
```

Seq. No.	402275
Seq. ID	LIB3431-051-P1-N1-E5
Method	BLASTX
NCBI GI	g1070408
BLAST score	166
E value	1.0e-11
Match length	47
% identity	74
NCBI Description	ferredoxin [2Fe-2S] I - rice

Seq. No.	402276
Seq. ID	LIB3431-051-P1-N1-E7
Method	BLASTX

Seq. No. 402394
 Seq. ID LIB3431-052-P1-N1-H7
 Method BLASTX
 NCBI GI g131176
 BLAST score 251
 E value 1.0e-21
 Match length 48
 % identity 98
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
 (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
 >gi_72683_pir_F1BH4 photosystem I chain IV precursor -
 barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
 -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A
 10.8kD photosystem I protein [Hordeum vulgare var.
 distichum]

Seq. No. 402395
 Seq. ID LIB3431-052-P1-N1-H9
 Method BLASTX
 NCBI GI g3183079
 BLAST score 209
 E value 1.0e-16
 Match length 54
 % identity 76
 NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
 >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate
 dehydrogenase [Oryza sativa]

Seq. No. 402396
 Seq. ID LIB3431-053-P1-K1-A1
 Method BLASTX
 NCBI GI g871931
 BLAST score 387
 E value 2.0e-37
 Match length 78
 % identity 99
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 402397
 Seq. ID LIB3431-053-P1-K1-A10
 Method BLASTX
 NCBI GI g729479
 BLAST score 667
 E value 1.0e-72
 Match length 147
 % identity 82
 NCBI Description FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_551131
 (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]

Seq. No. 402398
 Seq. ID LIB3431-053-P1-K1-A11
 Method BLASTX
 NCBI GI g131225
 BLAST score 322
 E value 3.0e-30
 Match length 71
 % identity 87

Seq. No. 402413
 Seq. ID LIB3431-053-P1-K1-B9
 Method BLASTX
 NCBI GI g1835731
 BLAST score 319
 E value 1.0e-29
 Match length 66
 % identity 95
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 402414
 Seq. ID LIB3431-053-P1-K1-C1
 Method BLASTX
 NCBI GI g5734636
 BLAST score 297
 E value 8.0e-27
 Match length 106
 % identity 50
 NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No. 402415
 Seq. ID LIB3431-053-P1-K1-C11
 Method BLASTX
 NCBI GI g2130042
 BLAST score 688
 E value 1.0e-72
 Match length 149
 % identity 92
 NCBI Description Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916) protoporphyrin IX Mg-chelatase subunit precursor [Hordeum vulgare]

Seq. No. 402416
 Seq. ID LIB3431-053-P1-K1-C12
 Method BLASTX
 NCBI GI g115772
 BLAST score 675
 E value 4.0e-71
 Match length 136
 % identity 94
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108 (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa]

Seq. No. 402417
 Seq. ID LIB3431-053-P1-K1-C2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 194
 E value 6.0e-15
 Match length 52
 % identity 73
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

```
Seq. No.          402418
Seq. ID           LIB3431-053-P1-K1-C3
Method            BLASTX
NCBI GI           g132105
BLAST score       638
E value           1.0e-66
Match length      119
% identity        98
NCBI Description  RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. No.          402419
Seq. ID           LIB3431-053-P1-K1-C4
Method            BLASTN
NCBI GI           g6015437
BLAST score       36
E value           2.0e-10
Match length      36
% identity        100
NCBI Description   Homo sapiens PEX1 mRNA, complete cds
```

```
Seq. No.          402420
Seq. ID           LIB3431-053-P1-K1-C5
Method            BLASTN
NCBI GI           g6015437
BLAST score       36
E value           2.0e-10
Match length      36
% identity        100
NCBI Description   Homo sapiens PEX1 mRNA, complete cds
```

```
Seq. No.          402421
Seq. ID           LIB3431-053-P1-K1-C6
Method            BLASTX
NCBI GI           g82734
BLAST score       812
E value           4.0e-87
Match length      164
% identity        31
NCBI Description   ubiquitin precursor - maize (fragment)
                   >gi 226763 prf 1604470A poly-ubiquitin [Zea mays]
```

```
Seq. No.      402422
Seq. ID      LIB3431-053-P1-K1-C8
Method       BLASTX
NCBI GI      g320618
BLAST score   455
E value      2.0e-45
```


[illegible]

```
Seq. No.      402461
Seq. ID      LIB3431-053-P1-K1-H3
Method       BLASTX
NCBI GI      g4582459
BLAST score   329
E value      1.0e-30
Match length  98
% identity    63
NCBI Description (AC007071) putative RanBP7/importin protein [Arabidopsis
thaliana]
```

```
Seq. No.          402463
Seq. ID           LIB3431-053-P1-K1-H7
Method            BLASTX
NCBI GI           g5442410
BLAST score       380
E value           2.0e-36
Match length      133
% identity        58
NCBI Description   (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]
```

Seq. No. 402465


```
Seq. ID      LIB3431-053-P1-K1-H9
Method       BLASTX
NCBI GI      g3789952
BLAST score   469
E value      4.0e-47
Match length 107
% identity    87
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
sativa]
```

```
Seq. No.      402466
Seq. ID      LIB3431-053-P1-N1-A1
Method       BLASTN
NCBI GI      g218209
BLAST score   214
E value      1.0e-117
Match length  302
% identity    93
NCBI Description  Oryza sativa mRNA for the small subunit of
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
pOSSS2106
```

```
Seq. No.      402467
Seq. ID      LIB3431-053-P1-N1-A10
Method       BLASTX
NCBI GI      g729477
BLAST score   498
E value      3.0e-50
Match length  110
% identity    84
NCBI Description  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
                >gi_320548_pir_A44974 ferredoxin--NADP+ reductase (EC
                1.18.1.2) precursor - common ice plant >gi_167256 (M25528)
                ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
                [Mesembryanthemum crystallinum] >gi_226768_prf_1604475A
                ferredoxin NADP reductase [Mesembryanthemum crystallinum]
```

```
Seq. No.      402468
Seq. ID      LIB3431-053-P1-N1-A11
Method       BLASTX
NCBI GI      g131225
BLAST score   179
E value      4.0e-13
Match length  48
% identity    69
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
precursor - barley >gi_167087 (M61146) photosystem I
hydrophobic protein [Hordeum vulgare]
```

```
Seq. No.      402469
Seq. ID      LIB3431-053-P1-N1-A12
Method       BLASTX
NCBI GI      g115813
BLAST score   211
E value      8.0e-25
Match length  82
```


protease [Oryza sativa]

```
Seq. No.      402479
Seq. ID      LIB3431-053-P1-N1-B3
Method       BLASTX
NCBI GI      g4982478
BLAST score   168
E value      1.0e-11
Match length  47
% identity    68
NCBI Description (AF069441) putative leucyl tRNA synthetase [Arabidopsis
                thaliana]
```

```
Seq. No.      402481
Seq. ID      LIB3431-053-P1-N1-B8
Method       BLASTX
NCBI GI      g400983
BLAST score   250
E value      3.0e-21
Match length  70
% identity    69
NCBI Description  50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11)
>gi_279648_pir_R5SP11 ribosomal protein L11 precursor -
spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein
L11 [Spinacia oleracea]
```

```
Seq. No.      402483
Seq. ID       LIB3431-053-P1-N1-C10
Method        BLASTX
NCBI GI       g687677
BLAST score    235
E value       1.0e-19
Match length   51
% identity     88
NCBI Description (U19925) unknown [Arabidopsis thaliana]
```


NCBI GI g3885892
 BLAST score 302
 E value 2.0e-27
 Match length 61
 % identity 95
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402495
 Seq. ID LIB3431-053-P1-N1-E10
 Method BLASTX
 NCBI GI g5734636
 BLAST score 187
 E value 6.0e-16
 Match length 87
 % identity 49
 NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No. 402496
 Seq. ID LIB3431-053-P1-N1-E11
 Method BLASTX
 NCBI GI g4544390
 BLAST score 188
 E value 6.0e-14
 Match length 62
 % identity 50
 NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana]

Seq. No. 402497
 Seq. ID LIB3431-053-P1-N1-E2
 Method BLASTN
 NCBI GI g218209
 BLAST score 58
 E value 1.0e-23
 Match length 94
 % identity 90
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone POSSS2106

Seq. No. 402498
 Seq. ID LIB3431-053-P1-N1-E3
 Method BLASTN
 NCBI GI g2072726
 BLAST score 460
 E value 0.0e+00
 Match length 491
 % identity 99
 NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No. 402499
 Seq. ID LIB3431-053-P1-N1-E6
 Method BLASTX
 NCBI GI g482311
 BLAST score 420
 E value 4.0e-41
 Match length 84


```
% identity      99
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
                  (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
```

```
Seq. No.      402500
Seq. ID      LIB3431-053-P1-N1-E7
Method       BLASTX
NCBI GI      g4417296
BLAST score   163
E value      5.0e-22
Match length  78
% identity    59
NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]
               >gi_4587592_gb_AAD25820.1_AC007232_10 (AC007232) unknown
               protein [Arabidopsis thaliana]
```

Seq. No.	402501
Seq. ID	LIB3431-053-P1-N1-E9
Method	BLASTX
NCBI GI	g3885894
BLAST score	330
E value	2.0e-38
Match length	113
% identity	77
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

```
Seq. No.      402502
Seq. ID      LIB3431-053-P1-N1-F1
Method       BLASTX
NCBI GI      g2570511
BLAST score   163
E value      3.0e-22
Match length  67
% identity    78
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
```

```
Seq. No.          402503
Seq. ID           LIB3431-053-P1-N1-F10
Method            BLASTX
NCBI GI           g2501190
BLAST score       167
E value           6.0e-19
Match length      78
% identity        71
NCBI Description   THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                   >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
                   - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                   [Zea mays]
```

```
Seq. No.          402504
Seq. ID           LIB3431-053-P1-N1-F11
Method            BLASTX
NCBI GI           g115787
BLAST score       471
E value           4.0e-47
Match length      106
```



```
Seq. No.          402519
Seq. ID           LIB3431-053-P1-N1-G5
Method            BLASTX
NCBI GI           g4530591
BLAST score       483
E value           2.0e-48
Match length      116
% identity        74
NCBI Description  (AF132475) heme oxygenase 1 [Arabidopsis thaliana]
                  >gi_4530593_gb_AAD22108.1_ (AF132476) heme oxygenase 1
                  [Arabidopsis thaliana] >gi_4877362_dbj_BAA77758.1_
                  (AB021857) plastid heme oxygenase [Arabidopsis thaliana]
                  >gi_4877397_dbj_BAA77759.1_ (AB021858) plastid heme
                  oxygenase [Arabidopsis thaliana] >gi_4883666_gb_AAB95301.2_
                  (AC003105) heme oxygenase 1 (HO1) [Arabidopsis thaliana]
```

```
Seq. No.          402520
Seq. ID          LIB3431-053-P1-N1-G9
Method           BLASTX
NCBI GI          g115813
BLAST score      257
E value          2.0e-35
Match length     95
% identity       83
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III
                  chlorophyll_a/b-binding protein [Lycopersicon esculentum]
```

```
Seq. No.      402521
Seq. ID       LIB3431-053-P1-N1-H10
Method        BLASTX
NCBI GI       g671740
BLAST score    486
E value       7.0e-49
Match length   88
% identity     100
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]
```

```
Seq. No.      402522
Seq. ID      LIB3431-053-P1-N1-H12
Method       BLASTX
NCBI GI      g2384956
BLAST score   275
E value      1.0e-25
Match length  149
% identity    43
NCBI Description (AF022985) No definition line found [Caenorhabditis
                elegans]
```

```
Seq. No.          402523
Seq. ID           LIB3431-053-P1-N1-H2
Method            BLASTX
NCBI GI           g733454
BLAST score       310
E value           6.0e-45
Match length      102
```


% identity 94
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 402524
Seq. ID LIB3431-053-P1-N1-H5
Method BLASTX
NCBI GI g131225
BLAST score 318
E value 3.0e-37
Match length 101
% identity 81
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 402525
Seq. ID LIB3431-053-P1-N1-H6
Method BLASTX
NCBI GI g2499417
BLAST score 327
E value 2.0e-30
Match length 78
% identity 79
NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1085826_pir_S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No. 402526
Seq. ID LIB3431-053-P1-N1-H7
Method BLASTX
NCBI GI g5442410
BLAST score 157
E value 1.0e-15
Match length 109
% identity 43
NCBI Description (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No. 402527
Seq. ID LIB3431-053-P1-N1-H8
Method BLASTX
NCBI GI g132081
BLAST score 170
E value 2.0e-15
Match length 53
% identity 84
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_68093_pir_RKRZS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - rice >gi_20341_emb_CAA30393_ (X07515) ribulose bisphosphate carboxylase [Oryza sativa]

Seq. No. 402528
Seq. ID LIB3431-053-P1-N1-H9
Method BLASTN

Method BLASTX
 NCBI GI g2435519
 BLAST score 388
 E value 2.0e-37
 Match length 117
 % identity 64
 NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW:P34110) [Arabidopsis thaliana]

Seq. No. 402538
 Seq. ID LIB3431-054-P1-K1-B3
 Method BLASTX
 NCBI GI g461812
 BLAST score 245
 E value 1.0e-20
 Match length 94
 % identity 45
 NCBI Description CYTOCHROME P450 72A1 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No. 402539
 Seq. ID LIB3431-054-P1-K1-B4
 Method BLASTX
 NCBI GI g3126854
 BLAST score 629
 E value 9.0e-66
 Match length 126
 % identity 94
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402540
 Seq. ID LIB3431-054-P1-K1-B6
 Method BLASTX
 NCBI GI g2894534
 BLAST score 561
 E value 8.0e-58
 Match length 124
 % identity 88
 NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 402541
 Seq. ID LIB3431-054-P1-K1-B7
 Method BLASTX
 NCBI GI g3024871
 BLAST score 216
 E value 3.0e-17
 Match length 160
 % identity 34
 NCBI Description HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No. 402542


```

NCBI GI      g3927827
BLAST score  195
E value      7.0e-15
Match length 115
% identity   42
NCBI Description (AC005727) osmotin-like protein precursor [Arabidopsis
thaliana]

```

```
Seq. No.      402548
Seq. ID      LIB3431-054-P1-K1-C2
Method       BLASTX
NCBI GI      g2306981
BLAST score   441
E value      9.0e-44
Match length  125
% identity    74
NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]
```

```
Seq. No.          402549
Seq. ID          LIB3431-054-P1-K1-C3
Method           BLASTX
NCBI GI          g417260
BLAST score      421
E value          2.0e-41
Match length     128
% identity       66
NCBI Description  LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
```

```
Seq. No.          402550
Seq. ID           LIB3431-054-P1-K1-C4
Method            BLASTN
NCBI GI           g3885891
BLAST score       245
E value           1.0e-135
Match length      245
% identity        100
NCBI Description   Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                   mRNA, complete cds
```

Seq. No.	402551
Seq. ID	LIB3431-054-P1-K1-C5
Method	BLASTX
NCBI GI	g2832672
BLAST score	160
E value	1.0e-10
Match length	33
% identity	97
NCBI Description	(AL021712) nifU-like protein [Arabidopsis thaliana]

```
Seq. No.      402552
Seq. ID      LIB3431-054-P1-K1-C6
Method       BLASTN
NCBI GI      g1835730
BLAST score   120
E value      5.0e-61
```



```
Seq. No.      402583
Seq. ID      LIB3431-054-P1-K1-H1
Method       BLASTX
NCBI GI      g3912968
BLAST score   172
E value      3.0e-12
Match length  123
% identity    30
NCBI Description ALPHA-ADAPTIN HOMOLOG >gi_1890329_emb_CAA71991_ (Y11104)
              alpha-adaptin [Drosophila melanogaster]
```

```
Seq. No.          402584
Seq. ID           LIB3431-054-P1-K1-H11
Method            BLASTX
NCBI GI           g629670
BLAST score       348
E value           6.0e-33
Match length      94
% identity        68
NCBI Description   hypothetical protein - tomato
```

Seq. No.	402585
Seq. ID	LIB3431-054-P1-K1-H3
Method	BLASTX
NCBI GI	g3885894
BLAST score	398
E value	7.0e-39
Match length	90
% identity	87
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

```
Seq. No.          402586
Seq. ID           LIB3431-054-P1-K1-H6
Method            BLASTX
NCBI GI           g22380
BLAST score       512
E value           6.0e-52
Match length      127
% identity         80
NCBI Description  (X59714) CAAT-box DNA binding protein subunit B (NF-YB)
                  [Zea mays]
```

```
Seq. No.          402587
Seq. ID           LIB3431-054-P1-K1-H7
Method            BLASTX
NCBI GI           g320618
BLAST score       335
E value           3.0e-32
Match length      88
% identity        83
NCBI Description   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
```


E value	9.0e-22
Match length	64
% identity	80
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

```
Seq. No.      402641
Seq. ID      LIB3431-054-P1-N1-H4
Method       BLASTX
NCBI GI      g115802
BLAST score   191
E value      1.0e-14
Match length  37
% identity    97
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
CAB-36) (LHCP) >gi_100311_pir_S21827 chlorophyll
a/b-binding protein (cab-36) - common tobacco
>gi_19827_emb_CAA41188_(X58230) chlorophyll a/b binding
protein [Nicotiana tabacum]
```

```
Seq. No.      402642
Seq. ID      LIB3431-054-P1-N1-H6
Method       BLASTX
NCBI GI      g115840
BLAST score   322
E value      1.0e-29
Match length  81
% identity    75
NCBI Description CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y
PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN
SUBUNIT B)
```

```
Seq. No.          402643
Seq. ID           LIB3431-054-P1-N1-H7
Method            BLASTX
NCBI GI           g115787
BLAST score       410
E value           2.0e-70
Match length      144
% identity        96
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109_
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

Seq. No.	402644
Seq. ID	LIB3431-054-P1-N1-H8
Method	BLASTX
NCBI GI	g517500
BLAST score	389
E value	7.0e-49
Match length	126
% identity	83
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) -rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	402696
Seq. ID	LIB3431-055-P1-N1-H6
Method	BLASTX
NCBI GI	g671740
BLAST score	458
E value	1.0e-45
Match length	86
% identity	99

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

```
Seq. No.          402697
Seq. ID           LIB3431-055-P1-N1-H7
Method            BLASTX
NCBI GI           g4325041
BLAST score       632
E value           6.0e-66
Match length      140
% identity        90
```

NCBI Description (AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]

```
Seq. No.          402698
Seq. ID           LIB3431-055-P1-N1-H8
Method            BLASTX
NCBI GI           g3126854
BLAST score       251
E value           1.0e-29
Match length      69
% identity        100
```

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

```
Seq. No.          402699
Seq. ID           LIB3431-055-P1-N1-H9
Method            BLASTX
NCBI GI           g131225
BLAST score       495
E value           7.0e-50
Match length      125
% identity        78
```

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	402700
Seq. ID	LIB3431-055-P2-K1-A9

Method	BLASTX
NCBI GI	g3650033
BLAST score	293
E value	2.0e-42
Match length	153
% identity	61
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]

Seq. No.	402701
Seq. ID	LIB3431-055-P2-K1-B1
Method	BLASTN
NCBI GI	g218142
BLAST score	77
E value	2.0e-35
Match length	225
% identity	85
NCBI Description	Rice mRNA for aspartic proteinase, complete cds

```
Seq. No.      402702
Seq. ID      LIB3431-055-P2-K1-B10
Method       BLASTX
NCBI GI      g2072555
BLAST score   233
E value      6.0e-20
Match length  44
% identity    98
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
               >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
               protein [Oryza sativa]
```

```
Seq. No.      402703
Seq. ID       LIB3431-055-P2-K1-B5
Method        BLASTX
NCBI GI       g3328122
BLAST score   150
E value       1.0e-09
Match length  41
% identity    78
NCBI Description (AF073473) phosphoglycerate kinase precursor [Solanum
tuberosum]
```

```
Seq. No.      402704
Seq. ID       LIB3431-055-P2-K1-B8
Method        BLASTX
NCBI GI       g2407281
BLAST score    668
E value       2.0e-70
Match length  135
% identity    93
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
subunit [Oryza sativa]
```

```
Seq. No.      402705
Seq. ID      LIB3431-055-P2-K1-B9
Method       BLASTX
NCBI GI      g3914005
BLAST score  237
```


Seq. ID LIB3431-055-P2-K1-F9
 Method BLASTX
 NCBI GI g2407281
 BLAST score 645
 E value 1.0e-67
 Match length 122
 % identity 97
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 402717
 Seq. ID LIB3431-055-P2-K1-G10
 Method BLASTN
 NCBI GI g3075487
 BLAST score 99
 E value 1.0e-48
 Match length 123
 % identity 95
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No. 402718
 Seq. ID LIB3431-055-P2-K1-G2
 Method BLASTN
 NCBI GI g20262
 BLAST score 227
 E value 1.0e-125
 Match length 231
 % identity 100
 NCBI Description O.sativa light-induced mRNA

Seq. No. 402719
 Seq. ID LIB3431-055-P2-K1-H11
 Method BLASTX
 NCBI GI g3004565
 BLAST score 340
 E value 4.0e-32
 Match length 97
 % identity 66
 NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 402720
 Seq. ID LIB3431-055-P2-K1-H12
 Method BLASTX
 NCBI GI g4678920
 BLAST score 227
 E value 1.0e-18
 Match length 102
 % identity 48
 NCBI Description (AL049711) putative heat shock transcription factor [Arabidopsis thaliana]

Seq. No. 402721
 Seq. ID LIB3431-055-P2-K1-H2
 Method BLASTN
 NCBI GI g2773153
 BLAST score 171


```
BLAST score      235
E value         2.0e-19
Match length    44
% identity      100
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
sativa]
```

```
Seq. No.      402771
Seq. ID      LIB3431-056-P1-K1-F1
Method       BLASTX
NCBI GI      g115787
BLAST score   636
E value      2.0e-74
Match length  142
% identity    95
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

```
Seq. No.      402772
Seq. ID      LIB3431-056-P1-K1-F10
Method       BLASTX
NCBI GI      g1173347
BLAST score   605
E value      4.0e-63
Match length  117
% identity    95
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
               (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
               >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
               3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
               (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
               aestivum]
```

```
Seq. No.      402773
Seq. ID       LIB3431-056-P1-K1-F12
Method        BLASTX
NCBI GI       g3913808
BLAST score    477
E value        6.0e-48
Match length   102
% identity     88
NCBI Description  FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
SYNTHETASE) >gi_2429618_dbj_BAA22284_ (AB007120)
ferrochelatase [Oryza sativa]
```

```
Seq. No.      402774
Seq. ID      LIB3431-056-P1-K1-F2
Method       BLASTX
NCBI GI      g585350
BLAST score   384
E value      3.0e-37
Match length  109
% identity    68
NCBI Description CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
```


% identity 100
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402828
Seq. ID LIB3431-056-P1-N1-E1
Method BLASTX
NCBI GI g3789954
BLAST score 611
E value 2.0e-63
Match length 113
% identity 100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 402829
Seq. ID LIB3431-056-P1-N1-E11
Method BLASTX
NCBI GI g1076724
BLAST score 374
E value 8.0e-36
Match length 72
% identity 94
NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No. 402830
Seq. ID LIB3431-056-P1-N1-E12
Method BLASTX
NCBI GI g1084461
BLAST score 287
E value 1.0e-25
Match length 98
% identity 60
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No. 402831
Seq. ID LIB3431-056-P1-N1-E2
Method BLASTX
NCBI GI g115813
BLAST score 234
E value 2.0e-19
Match length 56
% identity 80
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402832
Seq. ID LIB3431-056-P1-N1-E7
Method BLASTX
NCBI GI g5733872
BLAST score 182
E value 2.0e-13
Match length 57
% identity 60
NCBI Description (AC007932) Similar to gi_4982048 ribosomal protein L18 from

[illegible]

```
Seq. No.          402846
Seq. ID           LIB3431-056-P1-N1-G2
Method            BLASTX
NCBI GI           g2072555
BLAST score       228
E value           1.0e-18
Match length      42
% identity        100
```


[illegible]

```
Seq. No.      402896
Seq. ID      LIB3431-058-P1-K1-D7
Method       BLASTX
NCBI GI      g2130043
BLAST score   600
E value      3.0e-62
Match length  145
% identity    82
NCBI Description  Mg-chelatase chain Xantha-h - barley (fragment) >gi 847873.
```


(U26545) Mg-chelatase subunit [Hordeum vulgare]

Seq. No. 402897
Seq. ID LIB3431-058-P1-K1-D8
Method BLASTX
NCBI GI g115787
BLAST score 679
E value 1.0e-71
Match length 152
% identity 89
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 402898
Seq. ID LIB3431-058-P1-K1-E10
Method BLASTX
NCBI GI g482311
BLAST score 551
E value 8.0e-57
Match length 109
% identity 96
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No. 402899
Seq. ID LIB3431-058-P1-K1-E12
Method BLASTN
NCBI GI g20243
BLAST score 145
E value 1.0e-75
Match length 169
% identity 95
NCBI Description O.sativa GP28 gene (partial)

Seq. No. 402900
Seq. ID LIB3431-058-P1-K1-E2
Method BLASTX
NCBI GI g543711
BLAST score 191
E value 2.0e-18
Match length 86
% identity 70
NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796_pir_S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140) brain specific protein [Oryza sativa]

Seq. No. 402901
Seq. ID LIB3431-058-P1-K1-E4
Method BLASTX
NCBI GI g132105
BLAST score 479
E value 3.0e-48
Match length 109

% identity	86
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No.	402935
Seq. ID	LIB3431-058-P1-N1-B11
Method	BLASTX
NCBI GI	g2582381
BLAST score	144
E value	1.0e-08
Match length	31
% identity	87
NCBI Description	(AF021220) cation-chloride co-transporter [Nicotiana tabacum]
Seq. No.	402936
Seq. ID	LIB3431-058-P1-N1-B12
Method	BLASTX
NCBI GI	g115793
BLAST score	396
E value	2.0e-38
Match length	78
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB) >gi_72749_pir_CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_ (X63197) type III LHCII CAB precursor protein [Hordeum vulgare]
Seq. No.	402937
Seq. ID	LIB3431-058-P1-N1-B2
Method	BLASTX
NCBI GI	g3924605
BLAST score	227
E value	8.0e-19
Match length	53
% identity	72
NCBI Description	(AF069442) putative inhibitor of apoptosis [Arabidopsis thaliana]
Seq. No.	402938
Seq. ID	LIB3431-058-P1-N1-B5
Method	BLASTX
NCBI GI	g115813
BLAST score	201
E value	2.0e-15
Match length	46
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.	402939
Seq. ID	LIB3431-058-P1-N1-B6
Method	BLASTX
NCBI GI	g4038663
BLAST score	282
E value	4.0e-38

NCBI GI g4218534
BLAST score 34
E value 2.0e-09
Match length 46
% identity 93
NCBI Description Triticum sp. mRNA for GRAB1 protein

Seq. No. 403007
Seq. ID LIB3431-059-P1-K1-C12
Method BLASTN
NCBI GI g3885891
BLAST score 141
E value 1.0e-73
Match length 141
% identity 100
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No. 403008
Seq. ID LIB3431-059-P1-K1-C3
Method BLASTX
NCBI GI g5734720
BLAST score 231
E value 4.0e-19
Match length 138
% identity 43
NCBI Description (AC008075) Contains PF_01426 BAH (bromo-adjacent homology) domain. ESTs gb_N96349, gb_T42710, gb_H77084, gb_AA395147 and gb_AA605500 come from this gene. [Arabidopsis thaliana]

Seq. No. 403009
Seq. ID LIB3431-059-P1-K1-C5
Method BLASTX
NCBI GI g1848214
BLAST score 197
E value 4.0e-15
Match length 49
% identity 73
NCBI Description (Y11210) uracil phosphoribosyltransferase [Nicotiana tabacum]

Seq. No. 403010
Seq. ID LIB3431-059-P1-K1-C6
Method BLASTX
NCBI GI g2570511
BLAST score 625
E value 2.0e-65
Match length 123
% identity 95
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 403011
Seq. ID LIB3431-059-P1-K1-C8
Method BLASTX
NCBI GI g3885894
BLAST score 436
E value 3.0e-43

(Cab27) mRNA, nuclear gene encoding chloroplast protein,
complete cds

Seq. No. 403055
Seq. ID LIB3431-059-P1-N1-A2
Method BLASTX
NCBI GI g1001355
BLAST score 192
E value 1.0e-14
Match length 57
% identity 61
NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]

Seq. No. 403056
Seq. ID LIB3431-059-P1-N1-A3
Method BLASTX
NCBI GI g3126854
BLAST score 211
E value 1.0e-19
Match length 66
% identity 79
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403057
Seq. ID LIB3431-059-P1-N1-A4
Method BLASTX
NCBI GI g548774
BLAST score 267
E value 2.0e-23
Match length 69
% identity 80
NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi_542158_pir_S38360 ribosomal
protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
ribosomal protein L7A [Oryza sativa]

Seq. No. 403058
Seq. ID LIB3431-059-P1-N1-A6
Method BLASTX
NCBI GI g4469021
BLAST score 287
E value 1.0e-25
Match length 71
% identity 76
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403059
Seq. ID LIB3431-059-P1-N1-A9
Method BLASTX
NCBI GI g289920
BLAST score 329
E value 1.0e-30
Match length 63
% identity 100
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
hirsutum]

Seq. No. 403060

Method BLASTX
 NCBI GI g3036951
 BLAST score 199
 E value 9.0e-19
 Match length 52
 % identity 98
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
 [Nicotiana sylvestris]

Seq. No. 403096
 Seq. ID LIB3431-059-P1-N1-F5
 Method BLASTX
 NCBI GI g671740
 BLAST score 336
 E value 2.0e-31
 Match length 64
 % identity 95
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 403097
 Seq. ID LIB3431-059-P1-N1-F7
 Method BLASTN
 NCBI GI g606816
 BLAST score 306
 E value 1.0e-172
 Match length 326
 % identity 98
 NCBI Description Oryza sativa chloroplast carbonic anhydrase mRNA, complete
 cds

Seq. No. 403098
 Seq. ID LIB3431-059-P1-N1-F8
 Method BLASTX
 NCBI GI g517500
 BLAST score 378
 E value 2.0e-36
 Match length 91
 % identity 81
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa
 protein [Zea mays] >gi_444338_prf__1906386A photosystem II
 OE17 protein [Pisum sativum]

Seq. No. 403099
 Seq. ID LIB3431-059-P1-N1-G11
 Method BLASTX
 NCBI GI g4079798
 BLAST score 326
 E value 3.0e-30
 Match length 65
 % identity 97
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza
 sativa]

Seq. No. 403100
 Seq. ID LIB3431-059-P1-N1-G2
 Method BLASTX


```

NCBI GI           g2244867
BLAST score       261
E value           1.0e-22
Match length      138
% identity        39
NCBI Description   (Z97337) hydroxynitrile lyase like protein [Arabidopsis
                  thaliana]

```

```
Seq. No.      403132
Seq. ID      LIB3431-060-P1-K1-D2
Method       BLASTX
NCBI GI      g266567
BLAST score   548
E value      3.0e-56
Match length  144
% identity    72
NCBI Description  MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR
                  (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)
                  >gi_421956_pir_S23558 mitochondrial processing peptidase
                  (EC 3.4.99.41) alpha chain precursor - potato
                  >gi_21493_emb_CAA46990_(X66284) mitochondrial processing
                  peptidase [Solanum tuberosum]
```

```
Seq. No.      403133
Seq. ID       LIB3431-060-P1-K1-D3
Method        BLASTX
NCBI GI       g4098647
BLAST score    652
E value       2.0e-68
Match length   131
% identity     88
NCBI Description (U80668) homogentisate 1,2-dioxygenase [Arabidopsis
                thaliana]
```

```
Seq. No.          403134
Seq. ID          LIB3431-060-P1-K1-D4
Method          BLASTX
NCBI GI         g733454
BLAST score      431
E value         1.0e-42
Match length     103
% identity       81
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                  [Zea mays]
```

```
Seq. No.      403135
Seq. ID      LIB3431-060-P1-K1-D5
Method       BLASTX
NCBI GI      g548605
BLAST score   534
E value      1.0e-54
Match length  133
% identity    82
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                >gi_539055_pir_A48527 photosystem I protein psaK precursor
                - barley >gi_304220 (L12707) photosystem I PSI-K subunit
```


General Information	
Item	Value
1. Name	John Doe
2. Address	123 Main St, New York, NY 10001
3. Phone	(212) 555-1234
4. Email	john.doe@example.com
5. Date of Birth	1980-01-01
6. Gender	Male
7. Occupation	Software Engineer
8. Education	B.S. in Computer Science
9. Marital Status	Single
10. Languages Spoken	English, Spanish
11. Hobbies	Reading, Hiking, Coding
12. Emergency Contact	Jane Doe (Mother), (212) 555-5678
13. Medical History	No known allergies, no chronic conditions
14. Insurance	ABC Health Insurance, Policy # 123456789
15. Signature	[Signature]
16. Date	2023-10-27

```
Seq. No.          403137
Seq. ID           LIB3431-060-P1-K1-D8
Method            BLASTX
NCBI GI           g4587579
BLAST score       251
E value           2.0e-21
Match length      143
% identity        35
NCBI Description   (AC006550) F1003.1 [Arabidopsis thaliana]
```

Seq. No.	403139
Seq. ID	LIB3431-060-P1-K1-E1
Method	BLASTX
NCBI GI	g4559358
BLAST score	341
E value	5.0e-32
Match length	97
% identity	63
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

```
Seq. No.      403141
Seq. ID      LIB3431-060-P1-K1-E2
Method       BLASTX
```


[illegible]

```
Seq. No.      403147
Seq. ID       LIB3431-060-P1-K1-F11
Method        BLASTX
NCBI GI       g3068713
BLAST score    549
E value       2.0e-56
Match length   139
% identity     76
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
```

Seq. No.	403149
Seq. ID	LIB3431-060-P1-K1-F4
Method	BLASTN
NCBI GI	g2062705
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

51835

% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.	403173
Seq. ID	LIB3431-060-P1-N1-A11
Method	BLASTX
NCBI GI	g417260
BLAST score	327
E value	2.0e-30
Match length	75
% identity	83
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]
Seq. No.	403174
Seq. ID	LIB3431-060-P1-N1-A3
Method	BLASTN
NCBI GI	g2073379
BLAST score	154
E value	3.0e-81
Match length	173
% identity	97
NCBI Description	Rice CP26 mRNA, partial sequence
Seq. No.	403175
Seq. ID	LIB3431-060-P1-N1-A4
Method	BLASTX
NCBI GI	g4098250
BLAST score	160
E value	7.0e-11
Match length	56
% identity	50
NCBI Description	(U76611) similar to Solanum tuberosum ci21A gene product encoded by the sequence presented in GenBank Accession Number U76610 [Solanum tuberosum]
Seq. No.	403176
Seq. ID	LIB3431-060-P1-N1-A6
Method	BLASTN
NCBI GI	g218207
BLAST score	279
E value	1.0e-156
Match length	291
% identity	99
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139
Seq. No.	403177
Seq. ID	LIB3431-060-P1-N1-B4
Method	BLASTN
NCBI GI	g11957
BLAST score	65
E value	5.0e-28
Match length	84
% identity	48

(U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No. 403236
Seq. ID LIB3431-061-P1-K1-C5
Method BLASTX
NCBI GI g417154
BLAST score 370
E value 1.0e-35
Match length 98
% identity 85
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock protein 82 - rice (strain Taichung Native One)
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No. 403237
Seq. ID LIB3431-061-P1-K1-C6
Method BLASTN
NCBI GI g218207
BLAST score 191
E value 1.0e-103
Match length 191
% identity 100
NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No. 403238
Seq. ID LIB3431-061-P1-K1-C7
Method BLASTX
NCBI GI g4850382
BLAST score 152
E value 7.0e-10
Match length 70
% identity 44
NCBI Description (AC007357) Similar to gb_D38124 EREBP-3 from Nicotiana tabacum and contains PF_00847 AP2 domain. [Arabidopsis thaliana]

Seq. No. 403239
Seq. ID LIB3431-061-P1-K1-C8
Method BLASTX
NCBI GI g3126854
BLAST score 670
E value 1.0e-70
Match length 126
% identity 100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403240
Seq. ID LIB3431-061-P1-K1-C9
Method BLASTX
NCBI GI g3158476
BLAST score 310
E value 9.0e-35
Match length 109
% identity 64


```
Seq. ID      LIB3431-061-P1-K1-E6
Method       BLASTX
NCBI GI      g115787
BLAST score   552
E value      1.0e-56
Match length  105
% identity    99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                protein 2R precursor - rice >gi_20182_emb_CAA32109
                (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                [Oryza sativa]
```

```
Seq. No.          403256
Seq. ID           LIB3431-061-P1-K1-E8
Method            BLASTX
NCBI GI           g1881585
BLAST score       187
E value           5.0e-14
Match length      44
% identity        80
NCBI Description   (U72489) remorin [Solanum tuberosum]
```

```
Seq. No.      403257
Seq. ID      LIB3431-061-P1-K1-E9
Method       BLASTX
NCBI GI      g401190
BLAST score   669
E value      2.0e-70
Match length  128
% identity    96
NCBI Description  THAUMATIN-LIKE PROTEIN PRECURSOR >gi_100715_pir_S25551
                thaumatin-like protein - rice >gi_20376_emb_CAA48278_
                (X68197) thaumatin-like protein [Oryza sativa]
```

Seq. No.	403258
Seq. ID	LIB3431-061-P1-K1-F10
Method	BLASTX
NCBI GI	g3775987
BLAST score	430
E value	2.0e-42
Match length	112
% identity	71
NCBI Description	(AJ010457) RNA helicase [Arabidopsis thaliana]

```
Seq. No.      403259
Seq. ID      LIB3431-061-P1-K1-F11
Method       BLASTX
NCBI GI      g131225
BLAST score   311
E value      1.0e-28
Match length  105
% identity    65
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
precursor - barley >gi_167087 (M61146) photosystem I
hydrophobic protein [Hordeum vulgare]
```


[illegible]

```
Seq. No.          403287
Seq. ID           LIB3431-062-P1-K1-A2
Method            BLASTX
NCBI GI           g419742
BLAST score       624
E value           3.0e-65
Match length      127
% identity        91
NCBI Description   protochlorophyllide reductase (EC 1.3.1.33) precursor -
                   loblolly pine
```

```
Seq. No.      403289
Seq. ID      LIB3431-062-P1-K1-A7
Method       BLASTX
NCBI GI      g1835731
BLAST score   180
E value      9.0e-14
Match length  44
% identity    80
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

Seq. No. 403291

0950401-101000

Method BLASTX
NCBI GI g1617197
BLAST score 298
E value 7.0e-27
Match length 76
% identity 75
NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 403297
Seq. ID LIB3431-062-P1-K1-B6
Method BLASTX
NCBI GI g2245015
BLAST score 463
E value 3.0e-46
Match length 107
% identity 80
NCBI Description (Z97341) glucosyltransferase like protein [Arabidopsis thaliana]

Seq. No. 403298
Seq. ID LIB3431-062-P1-K1-B7
Method BLASTX
NCBI GI g2286121
BLAST score 521
E value 5.0e-53
Match length 102
% identity 97
NCBI Description (U88068) sec14 like protein [Oryza sativa]

Seq. No. 403299
Seq. ID LIB3431-062-P1-K1-B8
Method BLASTX
NCBI GI g871931
BLAST score 248
E value 6.0e-21
Match length 75
% identity 68
NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 403300
Seq. ID LIB3431-062-P1-K1-C11
Method BLASTX
NCBI GI g115772
BLAST score 156
E value 6.0e-11
Match length 32
% identity 100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108 (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa]

Seq. No. 403301
Seq. ID LIB3431-062-P1-K1-C12
Method BLASTX
NCBI GI g5091520

BLAST score 204
 E value 6.0e-16
 Match length 130
 % identity 45
 NCBI Description (AB023482) ESTs AU058081(E30812), AU058365(E50679), AU030138(E50679) correspond to a region of the predicted gene.; Similar to Spinacia oleracea mRNA for proteasome 37kD subunit.(X96974) [Oryza sativa]

Seq. No. 403302
 Seq. ID LIB3431-062-P1-K1-C5
 Method BLASTX
 NCBI GI g132105
 BLAST score 553
 E value 7.0e-57
 Match length 120
 % identity 87
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403303
 Seq. ID LIB3431-062-P1-K1-C6
 Method BLASTX
 NCBI GI g1854378
 BLAST score 252
 E value 1.0e-25
 Match length 125
 % identity 56
 NCBI Description (AB001338) Sucrose-Phosphate Synthase [Saccharum officinarum]

Seq. No. 403304
 Seq. ID LIB3431-062-P1-K1-C7
 Method BLASTX
 NCBI GI g4972111
 BLAST score 546
 E value 6.0e-56
 Match length 151
 % identity 62
 NCBI Description (AL078579) protein phosphatase homolog (PPH1) [Arabidopsis thaliana]

Seq. No. 403305
 Seq. ID LIB3431-062-P1-K1-C9
 Method BLASTN
 NCBI GI g2072554
 BLAST score 188
 E value 1.0e-101
 Match length 196
 % identity 99

BLAST score	444
E value	2.0e-45
Match length	141
% identity	70
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	403312
Seq. ID	LIB3431-062-P1-K1-D5
Method	BLASTX
NCBI GI	g3290022
BLAST score	434
E value	9.0e-43
Match length	142
% identity	58
NCBI Description	(AF044173) cysteine synthase; CS-B; O-acetylserine (thiol) lyase; plastidic isoform [Solanum tuberosum]
Seq. No.	403313
Seq. ID	LIB3431-062-P1-K1-D7
Method	BLASTX
NCBI GI	g3201969
BLAST score	225
E value	2.0e-18
Match length	43
% identity	98
NCBI Description	(AF068332) submergence induced protein 2A [Oryza sativa]
Seq. No.	403314
Seq. ID	LIB3431-062-P1-K1-E1
Method	BLASTN
NCBI GI	g2624325
BLAST score	86
E value	9.0e-41
Match length	110
% identity	95
NCBI Description	Oryza sativa mRNA for glycine-rich RNA-binding protein (OsGRP1)
Seq. No.	403315
Seq. ID	LIB3431-062-P1-K1-E11
Method	BLASTN
NCBI GI	g218209
BLAST score	155
E value	1.0e-81
Match length	281
% identity	96
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone poSSS2106
Seq. No.	403316
Seq. ID	LIB3431-062-P1-K1-E12
Method	BLASTX
NCBI GI	g3618310
BLAST score	331
E value	6.0e-31

Match length	101
% identity	65
NCBI Description	(AB001883) zinc finger protein [Oryza sativa]
Seq. No.	403317
Seq. ID	LIB3431-062-P1-K1-E3
Method	BLASTX
NCBI GI	g320618
BLAST score	476
E value	8.0e-48
Match length	115
% identity	80
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]
Seq. No.	403318
Seq. ID	LIB3431-062-P1-K1-E4
Method	BLASTX
NCBI GI	g2832606
BLAST score	214
E value	5.0e-17
Match length	90
% identity	50
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292810_emb_CAA19800.1_ (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	403319
Seq. ID	LIB3431-062-P1-K1-E5
Method	BLASTX
NCBI GI	g2306981
BLAST score	409
E value	2.0e-44
Match length	98
% identity	91
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]
Seq. No.	403320
Seq. ID	LIB3431-062-P1-K1-E6
Method	BLASTX
NCBI GI	g4512705
BLAST score	483
E value	1.0e-48
Match length	144
% identity	69
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	403321
Seq. ID	LIB3431-062-P1-K1-E7
Method	BLASTX
NCBI GI	g2739375
BLAST score	197
E value	3.0e-15

Seq. No. 403331
Seq. ID LIB3431-062-P1-K1-G1
Method BLASTX
NCBI GI g2462834
BLAST score 293
E value 3.0e-26
Match length 106
% identity 57
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403332
Seq. ID LIB3431-062-P1-K1-G10
Method BLASTN
NCBI GI g1835730
BLAST score 156
E value 1.0e-82
Match length 164
% identity 99
NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No. 403333
Seq. ID LIB3431-062-P1-K1-G11
Method BLASTX
NCBI GI g3126854
BLAST score 289
E value 2.0e-26
Match length 57
% identity 98
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403334
Seq. ID LIB3431-062-P1-K1-G12
Method BLASTX
NCBI GI g3885892
BLAST score 667
E value 3.0e-70
Match length 136
% identity 94
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 403335
Seq. ID LIB3431-062-P1-K1-G2
Method BLASTX
NCBI GI g5031281
BLAST score 356
E value 1.0e-33
Match length 121
% identity 60
NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 403336
Seq. ID LIB3431-062-P1-K1-G3
Method BLASTX
NCBI GI g2072555
BLAST score 237

E value 1.0e-123
 Match length 352
 % identity 91
 NCBI Description Oryza sativa ferredoxin mRNA, complete cds

Seq. No. 403362
 Seq. ID LIB3431-062-P1-N1-B9
 Method BLASTX
 NCBI GI g132105
 BLAST score 411
 E value 4.0e-40
 Match length 76
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403363
 Seq. ID LIB3431-062-P1-N1-C11
 Method BLASTX
 NCBI GI g115787
 BLAST score 403
 E value 3.0e-39
 Match length 76
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 403364
 Seq. ID LIB3431-062-P1-N1-C12
 Method BLASTN
 NCBI GI g20262
 BLAST score 108
 E value 1.0e-53
 Match length 220
 % identity 87
 NCBI Description O.sativa light-induced mRNA

Seq. No. 403365
 Seq. ID LIB3431-062-P1-N1-C5
 Method BLASTN
 NCBI GI g218207
 BLAST score 256
 E value 1.0e-142
 Match length 284
 % identity 98
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone

Demographic Characteristics	
Characteristic	Percentage
Age (years)	
< 18	12.5
18-24	28.3
25-34	21.7
35-44	18.9
45-54	15.6
55-64	10.2
65+	3.8
Gender	
Male	52.1
Female	47.9
Ethnicity	
White	68.4
Black	22.1
Hispanic	8.7
Other	2.8
Marital Status	
Married	55.3
Single	31.2
Divorced	12.8
Widowed	1.7
Education Level	
High School or Less	35.6
Some College	28.9
Bachelor's Degree	21.4
Graduate Degree	14.1
Income Level (Annual)	
< \$10,000	18.2
\$10,000-\$19,999	25.7
\$20,000-\$29,999	22.3
\$30,000-\$39,999	19.8
\$40,000-\$49,999	15.4
\$50,000-\$59,999	11.2
\$60,000-\$69,999	8.9
\$70,000-\$79,999	6.5
\$80,000-\$89,999	4.3
\$90,000-\$99,999	3.1
\$100,000+	2.6
Health Insurance Status	
Medicaid	32.1
Medicare	28.4
Private Insurance	21.7
Uninsured	17.8
Other	1.0
Employment Status	
Employed	45.3
Unemployed	31.2
Retired	18.9
Homemaker	3.8
Student	1.7
Other	0.1
Health Status	
Excellent	12.5
Very Good	28.3
Good	35.6
Fair	18.9
Poor	5.7
Chronic Conditions	
Hypertension	22.1
Diabetes	15.6
Heart Disease	18.9
Cholesterol	28.3
Asthma	12.5
Arthritis	21.7
Depression	15.6
Anxiety	12.5
Other	1.7
Healthcare Utilization	
Physician Visits (Last Year)	
< 1	12.5
1-2	28.3
3-4	35.6
5-6	18.9
7+	5.7
Emergency Room Visits (Last Year)	
0	45.3
1	28.3
2	18.9
3	8.7
4+	1.7
Prescription Medication (Last Year)	
0	12.5
1	28.3
2	35.6
3	18.9
4+	5.7
Healthcare Costs (Last Year)	
< \$1,000	12.5
\$1,000-\$1,999	28.3
\$2,000-\$2,999	35.6
\$3,000-\$3,999	18.9
\$4,000-\$4,999	5.7
\$5,000+	1.7

Seq. No. 403371

NCBI Description Oryza sativa mRNA for the small subunit of
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
pOSSS2106

Seq. No. 403381
Seq. ID LIB3431-062-P1-N1-E12
Method BLASTX
NCBI GI g3618310
BLAST score 378
E value 3.0e-36
Match length 72
% identity 100
NCBI Description (AB001883) zinc finger protein [Oryza sativa]

Seq. No. 403382
Seq. ID LIB3431-062-P1-N1-E2
Method BLASTX
NCBI GI g1617197
BLAST score 274
E value 4.0e-24
Match length 67
% identity 73
NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 403383
Seq. ID LIB3431-062-P1-N1-E3
Method BLASTX
NCBI GI g693920
BLAST score 386
E value 3.0e-37
Match length 77
% identity 95
NCBI Description (U21113) chlorophyll a/b binding protein [Solanum
tuberosum]

Seq. No. 403384
Seq. ID LIB3431-062-P1-N1-E5
Method BLASTX
NCBI GI g1076724
BLAST score 404
E value 3.0e-39
Match length 77
% identity 95
NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_(X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]

Seq. No. 403385
Seq. ID LIB3431-062-P1-N1-E7
Method BLASTX
NCBI GI g2739375
BLAST score 162
E value 6.0e-11
Match length 93
% identity 42
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

1997-1998		1998-1999		1999-2000		2000-2001		2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007		2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		2012-2013		2013-2014		2014-2015		2015-2016		2016-2017		2017-2018		2018-2019		2019-2020		2020-2021		2021-2022		2022-2023		2023-2024		2024-2025		2025-2026		2026-2027		2027-2028		2028-2029		2029-2030		2030-2031		2031-2032		2032-2033		2033-2034		2034-2035		2035-2036		2036-2037		2037-2038		2038-2039		2039-2040		2040-2041		2041-2042		2042-2043		2043-2044		2044-2045		2045-2046		2046-2047		2047-2048		2048-2049		2049-2050		2050-2051		2051-2052		2052-2053		2053-2054		2054-2055		2055-2056		2056-2057		2057-2058		2058-2059		2059-2060		2060-2061		2061-2062		2062-2063		2063-2064		2064-2065		2065-2066		2066-2067		2067-2068		2068-2069		2069-2070		2070-2071		2071-2072		2072-2073		2073-2074		2074-2075		2075-2076		2076-2077		2077-2078		2078-2079		2079-2080		2080-2081		2081-2082		2082-2083		2083-2084		2084-2085		2085-2086		2086-2087		2087-2088		2088-2089		2089-2090		2090-2091		2091-2092		2092-2093		2093-2094		2094-2095		2095-2096		2096-2097		2097-2098		2098-2099		2099-2100		2100-2101		2101-2102		2102-2103		2103-2104		2104-2105		2105-2106		2106-2107		2107-2108		2108-2109		2109-2110		2110-2111		2111-2112		2112-2113		2113-2114		2114-2115		2115-2116		2116-2117		2117-2118		2118-2119		2119-2120		2120-2121		2121-2122		2122-2123		2123-2124		2124-2125		2125-2126		2126-2127		2127-2128		2128-2129		2129-2130		2130-2131		2131-2132		2132-2133		2133-2134		2134-2135		2135-2136		2136-2137		2137-2138		2138-2139		2139-2140		2140-2141		2141-2142		2142-2143		2143-2144		2144-2145		2145-2146		2146-2147		2147-2148		2148-2149		2149-2150		2150-2151		2151-2152		2152-2153		2153-2154		2154-2155		2155-2156		2156-2157		2157-2158		2158-2159		2159-2160		2160-2161		2161-2162		2162-2163		2163-2164		2164-2165		2165-2166		2166-2167		2167-2168		2168-2169		2169-2170		2170-2171		2171-2172		2172-2173		2173-2174		2174-2175		2175-2176		2176-2177		2177-2178		2178-2179		2179-2180		2180-2181		2181-2182		2182-2183		2183-2184		2184-2185		2185-2186		2186-2187		2187-2188		2188-2189		2189-2190		2190-2191		2191-2192		2192-2193		2193-2194		2194-2195		2195-2196		2196-2197		2197-2198		2198-2199		2199-2200		2200-2201		2201-2202		2202-2203		2203-2204		2204-2205		2205-2206		2206-2207		2207-2208		2208-2209		2209-2210		2210-2211		2211-2212		2212-2213		2213-2214		2214-2215		2215-2216		2216-2217		2217-2218		2218-2219		2219-2220		2220-2221		2221-2222		2222-2223		2223-2224	
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Seq. No.      403517
Seq. ID       LIB3431-063-P1-N1-H5
Method        BLASTX
NCBI GI       g131225
BLAST score    216
E value       2.0e-17
Match length   56
% identity     73
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